

GenCore version 4.5  
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OW protein - protein search, using sw model

Run on: April 24, 2001, 15:31:29 ; Search time 26.96 Seconds  
(without alignments)  
657.660 Million cell updates/sec

Title: US-09-508-849-1

Perfect score: 1411

Sequence: 1 MQQPNVYPYPOIYWVDSAS.....SELVLNFEESQTFGLYKL 258

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1389.5	98.5	281	2	I38707	Fas ligand - human
2	1075.5	76.2	279	2	A53062	Fas ligand - mouse
3	1061	75.2	278	2	A49266	Fas ligand - rat
4	211	15.0	202	1	JN0869	tumor necrosis fac
5	208	14.7	202	1	B27303	tumor necrosis fac
6	204.5	14.5	197	1	JH0309	tumor necrosis fac
7	192	13.6	232	1	S12606	tumor necrosis fac
8	190.5	13.5	204	1	S24641	lymphotoxin - Dovi
9	190.5	13.5	233	1	QW4642	tumor necrosis fac
10	187	13.3	205	1	SMHUX	lymphotoxin alpha
11	185	13.1	204	1	S17289	tumor necrosis fac
12	181	12.8	234	1	J01344	tumor necrosis fac
13	177	12.5	141	2	A34043	hypothetical proli
14	172.5	12.2	233	1	QW4642	tumor necrosis fac
15	172.5	12.2	389	2	S27200	proline-rich prote
16	172	12.2	599	2	T10798	phosphorin-S - Vo
17	170.5	12.1	233	1	S22052	tumor necrosis fac
18	169.5	12.0	185	2	S52715	tumor necrosis fac
19	169.5	12.0	234	1	A25451	tumor necrosis fac
20	169.5	12.0	485	2	A33647	sulfated surface g
21	169	12.0	234	1	JH0529	tumor necrosis fac
22	167	11.8	415	1	A34170	acrosin (EC 3.4.21
23	165.5	11.7	235	2	S15490	tumor necrosis fac
24	163.5	11.6	233	2	S11688	tumor necrosis fac
25	163.5	11.6	235	1	QW4642	tumor necrosis fac
26	163	11.6	431	2	S47538	acrosin (EC 3.4.21
27	162	11.5	639	2	G02919	transcription fact
28	161.5	11.4	193	2	S06192	tumor necrosis fac
29	161	11.4	502	2	A55197	Wiskott-Aldrich sy

30	161	11.4	1206	2	S24407	formin isoform IV
31	161	11.4	1468	2	S11515	formin - mouse
32	159	11.3	464	2	S22697	extensin - Volvox
33	158.5	11.2	421	1	S11674	acrosin (EC 3.4.21
34	155.5	11.0	235	2	JU0029	tumor necrosis fac
35	155.5	11.0	440	2	I49681	glyceraldehyde-3-p
36	153.5	10.9	439	2	S51939	chitinase (EC 3.2.
37	153	10.8	760	2	T06291	extensin homolog T
38	152	10.8	487	2	S42442	nuclear protein EB
39	151	10.7	196	2	B48232	cysteine-rich exte
40	151	10.7	306	2	I49139	lymphotoxin-beta -
41	151	10.7	980	2	S54986	regulatory protein
42	150.5	10.7	1255	2	T31065	diaphanous protein
43	149.5	10.6	505	2	S72273	actin-depolymerizi
44	149.5	10.6	645	2	A71416	hypothetical prote
45	149.5	10.6	1171	2	T17454	diaphanous-related

## ALIGNMENTS

RESULT 1  
I38707  
Fas ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence.revision 29-May-1998 #text.change 21-Jul-2000  
C:Accession: I38707; J02340; S57565; I38554  
R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.  
Int. Immunol. 6, 1567-1574, 1994  
A:Title: Human Fas ligand: gene structure, chromosomal location and species specific  
A:Reference number: I38707; MUID:95127560  
A:Accession: I38707  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-281 <RES>  
A:Cross-references: EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:9595431  
R:Mita, E.; Hayashi, N.; Ito, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, Biochem. Biophys. Res. Commun. 204, 468-474, 1994  
A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.  
A:Reference number: J02340; MUID:95071350  
A:Accession: J02340  
A:Molecule type: DNA  
A:Residues: 1-281 <MIT>  
A:Cross-references: GB:D38122; DDBJ:D29820; NID:9601892; PIDN:BA07320.1; PID:q136990  
R:Schatzlein, C.E.  
Submitted to the EMBL Data Library, June 1995  
A:Reference number: S57565  
A:Accession: S57565  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-281 <SCH>  
A:Cross-references: EMBL:X89102; NID:9887455; PID:9887456  
R:Alderson, M.R.; Tough, T.W.; Davys-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; J. Exp. Med. 181, 71-77, 1995  
A:Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.  
A:Reference number: I38554; MUID:95105731  
A:Accession: I38554  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-281 <RE2>  
A:Cross-references: EMBL:U08137; NID:9624627; PIDN:AAC50071.1; PID:9624628  
C:Genetics:  
A:Gene: FasL  
A:Introns: 151/1; 116/3  
C:Keywords: glycoprotein; transmembrane protein  
F:80-102/Domain: transmembrane #status predicted <TM>  
F:76,184,250,260/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.5%; Score 1389.5; DB 2; Length 281;  
Best Local Similarity 91.8%; Pred. No. 2.3e-94;  
Matches 258; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

QY 1 MOOPFNYPTQIYWDSSASSPWAPPGIVLPCTSVPRRPGORRRPPPPPPPPPPPP 60  
 DB 1 MOOPFNYPTQIYWDSSASSPWAPPGIVLPCTSVPRRPGORRRPPPPPPPPPPPP 60  
 QY 61 PPLPPLPPLPKRGNHSGICLLVMEFVVALVGLGIMQFLHLOKE----- 110  
 DB 61 PPLPPLPPLPKRGNHSGICLLVMEFVVALVGLGIMQFLHLOKE----- 110  
 QY 111 -----PSPPEKKELRKVAHLTGKSNRSMPLMEDTYGIYLLSGVYKKG 157  
 DB 121 MHTASSLEKQIGHSPPEKKELRKVAHLTGKSNRSMPLMEDTYGIYLLSGVYKKG 180  
 QY 158 LYINETGLFYVSKYFRGOSCNPLPSHKYVRNSKYPQDLYVMGKMMSTCTTGOMA 217  
 DB 181 LYINETGLFYVSKYFRGOSCNPLPSHKYVRNSKYPQDLYVMGKMMSTCTTGOMA 240  
 QY 218 RSSYLGAVNLTADHLVYNVSELVNFEESSOTFFGLYKL 258  
 DB 241 RSSYLGAVNLTADHLVYNVSELVNFEESSOTFFGLYKL 281

F 2  
 A 22  
 Fas ligand - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: A53062  
 R:Takehashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag  
 Cell 76, 969-976, 1994  
 A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in  
 A:Reference number: A53062; M0ID:94185175  
 A:Accession: A53062  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-279 <TAK>  
 A:Cross-references: GB:006948; NID:9473564; PIDN:AAAI7800.1; PID:9473565

Query Match 76.2%; Score 1075.5; DB 2; Length 279;  
 Best Local Similarity 72.3%; Pred. No. 1.7e-71;  
 Matches 204; Conservative 23; Mismatches 28; Indels 27; Gaps 4;

QY 1 MOOPFNYPTQIYWDSSASSPWAPPGIVLPCTSVPRRPGORRRPPPPPPPPPPPP 59  
 DB 1 MOOPFNYPTQIYWDSSASSPWAPPGIVLPCTSVPRRPGORRRPPPPPPPPPPPP 60  
 QY 60 PPLPPLPPLPKRGNHSGICLLVMEFVVALVGLGIMQFLHLOKE----- 110  
 DB 61 PPLPPLPPLPKRGNHSGICLLVMEFVVALVGLGIMQFLHLOKE----- 117  
 QY 111 -----PSPPEKKELRKVAHLTGKSNRSMPLMEDTYGIYLLSGVYKKG 156  
 DB 118 -----PSPPEKKELRKVAHLTGKSNRSMPLMEDTYGIYLLSGVYKKG 177  
 QY 157 GLVINTGLFYVSKYFRGOSCNPLPSHKYVRNSKYPQDLYVMGKMMSTCTTGOMA 216  
 DB 178 GLVINTGLFYVSKYFRGOSCNPLPSHKYVRNSKYPQDLYVMGKMMSTCTTGOMA 237  
 QY 217 ARSSYLGAVNLTADHLVYNVSELVNFEESSOTFFGLYKL 258  
 DB 238 ARSSYLGAVNLTADHLVYNVSELVNFEESSOTFFGLYKL 279

RESULT 3

A49266  
 fas ligand - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: A49266  
 R:Suda, T.; Takehashi, T.; Golstein, P.; Nagata, S.  
 Cell 75, 1169-1178, 1993  
 A:Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor  
 A:Reference number: A49266; M0ID:94084792

A:Accession: A49266  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-278 <SUD>  
 A:Cross-references: GB:003470; NID:9440178; PIDN:AAC52129.1; PID:9440179  
 C:Keywords: glycoprotein; transmembrane protein

Query Match 75.2%; Score 1061; DB 2; Length 278;  
 Best Local Similarity 72.0%; Pred. No. 2e-70;  
 Matches 203; Conservative 19; Mismatches 32; Indels 28; Gaps 4;

QY 1 MOOPFNYPTQIYWDSSASSPWAPPGIVLPCTSVPRRPGORRRPPPPPPPPPPPP 59  
 DB 1 MOOPFNYPTQIYWDSSASSPWAPPGIVLPCTSVPRRPGORRRPPPPPPPPPPPP 60  
 QY 60 PPLPPLPPLPKRGNHSGICLLVMEFVVALVGLGIMQFLHLOKE----- 110  
 DB 61 PPLPPLPPLPKRGNHSGICLLVMEFVVALVGLGIMQFLHLOKE----- 116  
 QY 111 -----PSPPEKKELRKVAHLTGKSNRSMPLMEDTYGIYLLSGVYKKG 156  
 DB 117 HSLRVSSFEKQIANPSTPSPTKKPRSAHLTGKSNRSMPLMEDTYGIYLLSGVYKKG 176  
 QY 157 GLVINTGLFYVSKYFRGOSCNPLPSHKYVRNSKYPQDLYVMGKMMSTCTTGOMA 216  
 DB 177 GLVINTGLFYVSKYFRGOSCNPLPSHKYVRNSKYPQDLYVMGKMMSTCTTGOMA 236  
 QY 217 ARSSYLGAVNLTADHLVYNVSELVNFEESSOTFFGLYKL 258  
 DB 237 ARSSYLGAVNLTADHLVYNVSELVNFEESSOTFFGLYKL 278

RESULT 4

JN0869  
 tumor necrosis factor beta - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: JN0869  
 R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.  
 Gene 132, 227-236, 1993  
 A:Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding gene  
 A:Reference number: JN0869; M0ID:94040766  
 A:Accession: JN0869  
 A:Molecule type: DNA  
 A:Residues: 1-202 <KWO>  
 A:Cross-references: GB:L00981; NID:9205253; PIDN:AAI16276.1; PID:9205255  
 A:Note: the authors translated codon CTC for residue 172 as Tle  
 C:Comment: This protein is structurally related pleiotropic cytokinase with overlap  
 C:Keywords: tumor necrosis factor

Query Match 15.0%; Score 211; DB 1; Length 202;  
 Best Local Similarity 31.7%; Pred. No. 1.2e-08;  
 Matches 58; Conservative 30; Mismatches 81; Indels 14; Gaps 3;

QY 90 VLVALVGLGIMQFL-----PHLOKEPSPPPEKK-----ELRKVAHLTGKSNRSMPLMED 141  
 DB 20 LIGLLALPLPQAGQISGVFSSASRTAHPQKHLTGKLPAAHLVGYPSKNSLIMRAN 79  
 QY 142 TYGIVLLSGVYKKGGLVYNGLFYVSKYFRGOSCN-----NLPLPSHKYVRNSKY 195  
 DB 80 TDRAPLRHGFSLNNNSLLIPTSGLYFVYQVVFSSCSPPRAIPRIYLAHEVQLFSSQY 139  
 QY 196 PODLYVMGKMMSTCTTGOMARSSYLGAVNLTADHLVYNVSELVNFEESSOTFFGL 255  
 DB 140 PFRVPLPSAQKSVYRPLQDGPWRSMQGAVALFLSKDQLSTHTDGLSHLHFSSTVFPGA 199  
 QY 256 YKL 258

Db 200 FALL 202

RESULT 5  
B27303

tumor necrosis factor beta precursor - mouse

N:Alternate names: lymphotoxin; TNF beta

C:Species: Mus musculus (house mouse)

C&gt;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 24-Sep-1999

C:Accession: B27303; S01342; S10083; I56004; I48853; I55980

R:Semom, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.

Nucleic Acids Res. 15, 9083-9084, 1987

A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tumor necrosis factor) gene

A:Reference number: A93679; MUID:88067722

A:Accession: B27303

A:Molecule type: DNA

A:Residues: 1-202 &lt;SEM&gt;

A:Cross-references: GB:Y00467; NID:954830; PIDN:CAA68529.1; PID:954831

Nucleic Acids Res. 14, 7713-7725, 1986

A:Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are

A:Reference number: S01342; MUID:87040736

A:Accession: S01342

A:Molecule type: DNA

A:Residues: 1-11; 139-160; 'CG', 163-178 &lt;NED&gt;

A:Cross-references: EMBL:X06217

A:Accession: S10083

A:Molecule type: mRNA

A:Residues: 6-202 &lt;MEI&gt;

A:Cross-references: EMBL:X14800; NID:954833; PIDN:CAA32906.1; PID:9736269

R:Gardner, S.M.; Mock, B.A.; Hlilgers, J.; Huppi, K.E.; Roeder, W.D.

J. Immunol. 139, 476-483, 1987

A:Title: Mouse lymphotoxin and tumor necrosis factor: structural analysis of the cloned

A:Reference number: I56004; MUID:87252204

A:Accession: I56004

A:Molecule type: translated from GB/EMBL/DBJ

A:Residues: 1-25; 'P', 27-202 &lt;RES&gt;

A:Cross-references: GB:M17015; NID:9198880; PIDN:AAA39450.1; PID:9387407

R:Gray, P.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddle, N.

Nucleic Acids Res. 15, 3937, 1987

A:Title: The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.

A:Reference number: I48853; MUID:87231097

A:Accession: I48853

A:Molecule type: translated from GB/EMBL/DBJ

A:Residues: 1-202 &lt;RE2&gt;

A:Cross-references: EMBL:Y00137; NID:954842; PIDN:CAA68330.1; PID:954843

R:Li, C.

J. Immunol. 138, 4496-4501, 1987

A:Title: Cloning and expression of murine lymphotoxin cDNA.

A:Reference number: I55980; MUID:87224127

A:Accession: I55980

A:Molecule type: translated from GB/EMBL/DBJ

A:Residues: 1-202 &lt;RE3&gt;

A:Cross-references: GB:M16819; NID:9202088; PIDN:AAA40460.1; PID:9202089

C:Comment: The first intron occurs in the 5'-untranslated region.

C:Genetics:

A:Gene: Tnf

A:Map position: 17

A:Introns: 32/3; 66/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

Query Match 14.7%; Score 208; DB 1; Length 202;  
Best Local Similarity 31.7%; Pred. No. 1.9e-08;

Matches 58; Conservative 29; Mismatches 82; Indels 14; Gaps 3;

QY 90 VLVAVGLGFMFOL-----FHQKPPPEPK-----ELKRAHLTGKSNKSNLEMD 141

Db 20 ILGLLLALPLGAQGLSGVFSAPRAHPLPKHLTHGLKPAHLVGVPSKONSLMRAS 79

QY 142 TYGIYLLSGVKKKGGVYINFTGLFYVSKYFRGOSCN-----NLPISHVYRNKY 195

Db 80 TDRALRHGFSLSNNSLIPITSGLIFYVSOVFSGSCSPRAIPPIYLAHEVOLFFSOY 139

QY 196 PDLYMEGRKMSYCTTGOMARSSYLGAVENTSADHLVYVSELVLNFEESQTFPGL 255

Db 140 PPHVPLLSAQSKSVYVGLGQPVWRSMYQGAVFLLSKGDQSTHTDGIHSHFSPSVFFGA 199

QY 256 YKL 258

Db 200 FALL 202

RESULT 6  
JH0309

tumor necrosis factor beta precursor - rabbit

N:Alternate names: lymphotoxin; TNF beta

C:Species: Oryctolagus cuniculus (domestic rabbit)

C&gt;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: JH0309; P00098

R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.

Gene 95, 215-221, 1990

A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding T

A:Reference number: JH0309; MUID:91065534

A:Accession: JH0309

A:Molecule type: DNA

A:Residues: 1-197 &lt;SH2&gt;

A:Cross-references: GB:M60340; GB:M35326; NID:9165754; PIDN:AAA31483.1; PID:9165755;

R:Shakhov, A.N.; Kuprash, D.V.; Turetskaya, R.L.; Azizov, M.M.; Andreyeva, A.V.; Nedo

Mol. Biol. (Mosk.) 23, 1743-1750, 1989

A:Title: Cloning and structural analysis of the genes, coding for rabbit tumor necro

A:Reference number: P00098; MUID:90220566

A:Accession: P00098

A:Molecule type: mRNA

A:Residues: 1-197 &lt;SHA&gt;

A:Cross-references: GB:X55745; NID:9297167; PIDN:CAA39275.1; PID:9297168

C:Genetics:

A:Introns: 25/3; 61/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

F:1-26/Domain: signal sequence #status predicted &lt;SIG&gt;

F:27-197/Product: lymphotoxin #status predicted &lt;MAT&gt;

Query Match 14.5%; Score 204.5; DB 1; Length 197;  
Best Local Similarity 27.3%; Pred. No. 3.3e-08;

Matches 66; Conservative 28; Mismatches 93; Indels 55; Gaps 7;

QY 25 PGTVLPCTSVPRRRGRRPPPPPPPLPLPLPLKRGHSGGLCL 84

Db 3 PPGRLY-----LPRLGLLAPPPGAGLPPRAEPSPSARAQAORLQKHGHST----- 52

QY 85 VWFVVALVGLGLGFMFOLFHQKPPPEPKELRYVAHLTGKSNKSNLEMD-DTY 143

Db 53 -----LKPAAHLVGPDSAD-SLRRAATD 76

QY 144 GIVLLSGVKKKGGVYINFTGLFYVSKYFRGOSCN-----NLPISHVYRNKY 197

Db 77 RAFLRHGFSLSNNSLIPITSGLIFYVSOVFSGSCSPRAIPPIYLAHEVOLFFSOY 136

QY 198 DLVMEGRKMSYCTTGOMARSSYLGAVENTSADHLVYVSELVLNFEESQTFPGL 255

Db 137 HVPPLLSAQ-KSVCPGPPGQPVWRSMYQGAVFLLSKGDQSTHTDGIHSHFSPSVFFGA 199

QY 257 KL 258

Db 196 AL 197

## RESULT 7

S12606

tumor necrosis factor alpha precursor - pig

C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000C:Accession: S12606; S17290; S18965; 146659  
R:Reviews, R.T.: Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.

Nucleic Acids Res. 18, 5564, 1990

A:Title: Gene sequence of porcine tumor necrosis factor alpha.

A:Reference number: S12606; MUID:91016861

A:Accession: S12606

A:Molecule type: DNA

A:Residues: 1-232 &lt;DRE&gt;

A:Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136

R:Kuhner, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal

A:Reference number: S17289; MUID:91340150

A:Accession: S17290

A:Molecule type: DNA

A:Residues: 1-232 &lt;KUH&gt;

A:Cross-references: EMBL:X54659; NID:g2132; PIDN:CAA38639.1; PID:g2134

A:Note: The authors translated the codon GAG for residue 202 as Gly

R:Choi, C.S.; Mollitor, T.W.; Lin, G.F.; Murttaugh, M.P.

submitted to the EMBL Data Library, January 1991

A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fa

A:Reference number: S18965

A:Accession: S18965

A:Molecule type: mRNA

A:Residues: 1-232 &lt;CHO&gt;

A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138

R:Pauli, U.; Beutler, B.; Peterhans, E.

Gene 81, 185-191, 1989

A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction

A:Reference number: 146659; MUID:90034181

A:Accession: 146659

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 44-232 &lt;PAU&gt;

A:Cross-references: GB:M29079; NID:g164694; PIDN:AAA1128.1; PID:g164695

C:Genetics: 62/3; 78/1; 93/1

A:Introns: 62/3; 78/1; 93/1

C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myr

F:1-77/Domain: propeptide #status predicted &lt;PRO&gt;

F:78-332/Product: tumor necrosis factor alpha #status predicted &lt;ANT&gt;

F:18-20/Binding site: myristate (Lys) (covalent) #status predicted

F:176/Disulfide bonds: #status predicted

Query Match 13.6%; Score 192; DB 1; Length 232;

Best Local Similarity 31.3%; Pred. No. 3.2e-07;

Matches 68; Conservative 25; Mismatches 90; Indels 34; Gaps 11;

72 KKRGNSTGICLLVMEFVVALVGLGFMOLFHL-----QKE--PSP-----PEKKEL 120

20 KAGGPGSGSRRCCLSLSPFL--LVAGATTLFCLLHFVIGPQKEEPFAGLSINPLAOG 77

121 RK-----VAHLTGKSNRSRMPLEMDTYGIVLL-SGVKKYKGLVINEGLVYFVYSK 171

78 RSSQTSRDKRVAVHVNKKEGO-LQMOSGYANALLANGKELKDNDLVVPTDGLLYYSQ 136

172 VYFRGSC--NNPLSHKVMNRSKYPODLVMEGKMMSV-----TTGQMMARSSYL 222

137 VFRGGCGSTNFTLHTTTSRIAIVT-QTKVNLSAIKSCQRETPBGAERAKWPEPIYL 195

223 GAVFNLTSADHLVNVSELVNFEEES-QTFGLYKL 258

196 GGVFQLEKDRLSAELINLPDYLDFAESGGVYFGIALL 232

## RESULT 8

S24641

lymphotoxin - bovine

C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999C:Accession: I46046; S24641  
R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and

A:Reference number: I46046; MUID:94083525

A:Accession: I46046

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-204 &lt;CL2&gt;

A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797

C:Genetics: 32/3; 68/1

A:Introns: 32/3; 68/1

C:Superfamily: tumor necrosis factor

Query Match 13.5%; Score 190.5; DB 1; Length 204;

Best Local Similarity 30.3%; Pred. No. 3.6e-07;

Matches 60; Conservative 29; Mismatches 92; Indels 17; Gaps 6;

69 PPKRGNSTGICLLVMEFVVALVGLGFMOLFHLQKEPSPPPEKKELKRVANL 128

16 PLLLLG-----LLALPLAQLRGIGLTPSAQPAHQQLPFTROTTLKPAHLVG 68

129 KSNRSRMPLEME-DYTGIVLISGVKKKGGVINEGLVYFVYSKVFQSC-----NN 181

69 DPSTQD-SLEWRANTRAFLRHGFSLSNNSLVPVTGGLVYFVSQVVEFGCGCPRPATPP 127

182 LPLSHKYVMNRSKYPODLVMEGKMMSYCTTGQ-VMARSSYLCAVNLTSADHLVNVSE 240

128 LYLAHEVQLFSPYPRPHVPLLSNQ-KSVCPGPGPWHVRSYQGAVALTLRGDLSHTDGS 186

241 LSLVNEESQTFEGLYKL 258

187 ISHLLSPSSVFFGAFAL 204

Query Match 13.5%; Score 190.5; DB 1; Length 204;

Best Local Similarity 30.3%; Pred. No. 3.6e-07;

Matches 60; Conservative 29; Mismatches 92; Indels 17; Gaps 6;

69 PPKRGNSTGICLLVMEFVVALVGLGFMOLFHLQKEPSPPPEKKELKRVANL 128

16 PLLLLG-----LLALPLAQLRGIGLTPSAQPAHQQLPFTROTTLKPAHLVG 68

129 KSNRSRMPLEME-DYTGIVLISGVKKKGGVINEGLVYFVYSKVFQSC-----NN 181

69 DPSTQD-SLEWRANTRAFLRHGFSLSNNSLVPVTGGLVYFVSQVVEFGCGCPRPATPP 127

182 LPLSHKYVMNRSKYPODLVMEGKMMSYCTTGQ-VMARSSYLCAVNLTSADHLVNVSE 240

128 LYLAHEVQLFSPYPRPHVPLLSNQ-KSVCPGPGPWHVRSYQGAVALTLRGDLSHTDGS 186

241 LSLVNEESQTFEGLYKL 258

187 ISHLLSPSSVFFGAFAL 204

Query Match 13.5%; Score 190.5; DB 1; Length 204;

Best Local Similarity 30.3%; Pred. No. 3.6e-07;

Matches 60; Conservative 29; Mismatches 92; Indels 17; Gaps 6;

69 PPKRGNSTGICLLVMEFVVALVGLGFMOLFHLQKEPSPPPEKKELKRVANL 128

16 PLLLLG-----LLALPLAQLRGIGLTPSAQPAHQQLPFTROTTLKPAHLVG 68

129 KSNRSRMPLEME-DYTGIVLISGVKKKGGVINEGLVYFVYSKVFQSC-----NN 181

69 DPSTQD-SLEWRANTRAFLRHGFSLSNNSLVPVTGGLVYFVSQVVEFGCGCPRPATPP 127

182 LPLSHKYVMNRSKYPODLVMEGKMMSYCTTGQ-VMARSSYLCAVNLTSADHLVNVSE 240

128 LYLAHEVQLFSPYPRPHVPLLSNQ-KSVCPGPGPWHVRSYQGAVALTLRGDLSHTDGS 186

241 LSLVNEESQTFEGLYKL 258

187 ISHLLSPSSVFFGAFAL 204

Query Match 13.5%; Score 190.5; DB 1; Length 204;

Best Local Similarity 30.3%; Pred. No. 3.6e-07;

Matches 60; Conservative 29; Mismatches 92; Indels 17; Gaps 6;

69 PPKRGNSTGICLLVMEFVVALVGLGFMOLFHLQKEPSPPPEKKELKRVANL 128

16 PLLLLG-----LLALPLAQLRGIGLTPSAQPAHQQLPFTROTTLKPAHLVG 68

129 KSNRSRMPLEME-DYTGIVLISGVKKKGGVINEGLVYFVYSKVFQSC-----NN 181

69 DPSTQD-SLEWRANTRAFLRHGFSLSNNSLVPVTGGLVYFVSQVVEFGCGCPRPATPP 127

182 LPLSHKYVMNRSKYPODLVMEGKMMSYCTTGQ-VMARSSYLCAVNLTSADHLVNVSE 240

128 LYLAHEVQLFSPYPRPHVPLLSNQ-KSVCPGPGPWHVRSYQGAVALTLRGDLSHTDGS 186

241 LSLVNEESQTFEGLYKL 258

187 ISHLLSPSSVFFGAFAL 204

Query Match 13.5%; Score 190.5; DB 1; Length 204;

Best Local Similarity 30.3%; Pred. No. 3.6e-07;

Matches 60; Conservative 29; Mismatches 92; Indels 17; Gaps 6;

69 PPKRGNSTGICLLVMEFVVALVGLGFMOLFHLQKEPSPPPEKKELKRVANL 128

16 PLLLLG-----LLALPLAQLRGIGLTPSAQPAHQQLPFTROTTLKPAHLVG 68

129 KSNRSRMPLEME-DYTGIVLISGVKKKGGVINEGLVYFVYSKVFQSC-----NN 181

69 DPSTQD-SLEWRANTRAFLRHGFSLSNNSLVPVTGGLVYFVSQVVEFGCGCPRPATPP 127

182 LPLSHKYVMNRSKYPODLVMEGKMMSYCTTGQ-VMARSSYLCAVNLTSADHLVNVSE 240





A:Note: This protein was isolated from the monocyte-like cell line HL-60 from a promyel-  
R.Mang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsell, J.N.;  
Science 228, 149-154, 1985  
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
A:Reference number: A44189; MUID:85142190  
A:Molecule type: mRNA  
A:Residues: 1-62; 'S', 64-223 <NAN>  
A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738  
R:Fukuda, S.; Ando, S.; Sanou, O.; Tanial, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An-  
Lymphokine Res. 7, 175-185, 1988  
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and  
A:Reference number: A61478; MUID:88301617  
A:Accession: B61478  
A:Molecule type: protein  
A:Residues: 83-102;109-119,121-128, 'X',130-131,142-144, 'X',146, 'xxx',150-152,159-174;180  
R:Marmentou, A.; Franssen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,  
Eur. J. Biochem. 152, 515-522, 1985  
A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison  
A:Reference number: I53311; MUID:86030296  
A:Accession: I53311  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-233 <MAR>  
A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
A:Residues: 1-233 <MAR>  
A:Molecule type: DNA  
A:Experimental source: U-937 cells  
R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
Eur. J. Biochem. 235, 431-437, 1996  
A:Title: O-glycosylated species of natural human tumor-necrosis factor-alpha.  
A:Reference number: S62610; MUID:96202967  
A:Accession: S62610  
A:Molecule type: protein  
A:Residues: 77-99 <TAK>  
R:D'Alfonso, S.; Rlichardi, P.M.  
Immunogenetics 39, 150-154, 1994  
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region  
A:Reference number: I54522; MUID:94102809  
A:Accession: I54522  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-8 <DAL>  
A:Cross-references: GB:S68530; NID:g544751  
R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
J. Exp. Med. 176, 1053-1062, 1992  
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys-  
A:Reference number: A59163; MUID:93018820  
A:Status: annotation: identification of myristylated lysines  
R:Harwel, B.B.; Kohr, W.J.; Hase, P.E.; Moffatt, B.; Spencer, S.A.; Henzel, W.J.; Bring-  
J. Biol. Chem. 260, 2345-2354, 1985  
A:Title: Human tumor necrosis factor. Production, purification, and characterization.  
A:Reference number: A92511; MUID:85130974  
A:Contents: annotation: disulfide bond  
A:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction  
out detriment to normal cells. It can also act synergistically with interferon gamma to  
C:Comment: TNF-alpha and -beta (lymphokine) are the products of different genes closely  
ut are produced by different cell types and have different induction kinetics.  
C:Genetics:  
A:Gene: GDB:TNF; TNFA  
A:Cross-references: GDB:120441; OMIM:191160  
A:Map position: 6p21.3-6p21.3  
A:Introns: 62/3; 78/1; 94/1  
C:Complex: homotrimer  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macro-  
F:1-76/Domain: propeptide #status predicted <PRO>  
F:77-233/Product: tumor necrosis factor #status experimental <MAT>  
F:19-20/Binding site: myristate (lys) (covalent) #status experimental  
F:81/Binding site: carboxylate (ser) (covalent) (partial) #status experimental  
F:145-177/Disulfide bonds: #status experimental

Query Match	12.28;	Score 172.5;	DB 1;	Length 233;
Best Local Similarity	26.88;	Pred. No. 8.6e-06;		

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Matches 60; Conservative 30; Mismatches 91; Indels 43; Gaps 10;
OY 70 PLKRGHNHSTGCLLVFMFVVALVGLGMPQLFHL-----QKESP----- 113
Db 18 PKRTGGPGGSRCLFLSLFSFLI--VAGATTLFLCLHFGVIGPQREFFPRDLISPLAQ 75
OY 114 -----PPEKKELRKVAHLTGKNSRSMPLWEMEDTYGIYVL--SGVYKKKGGLVINEG 164
Db 76 AVRSSSRTPSDK----PVAHVANPQAEQ--LQWLRANALLAVGELRDNLVPSQG 130
OY 165 LFVYVSKVYFRGSC--NNLPLSHKVYWRNSKYPDDLVMMEGKMSYC-----TTGQM 215
Db 131 LYLISQVLFRGCGSPRHVLLTHIRISRIANSY-QTKNKLNSAIRSPQORETPBEAEKRP 189
OY 216 WARSSYLGAVENTLSADHLVYVNSLSLVNFEES-QTEFGLYKL 258
Db 190 WEPIYLGIVGFQLEKGRLSAEINRPDYLDFAESQVYFGIAL 233

RESULT 15
S27200
proline-rich protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S27200
R:Sazuka, T.; Tomooka, Y.; Kathju, S.; Ikawa, Y.; Noda, M.; Kumar, S.
Biochim. Biophys. Acta 1132, 240-248, 1992
A:Title: Identification of a developmentally regulated gene in the mouse central nerv
A:Reference number: S27200; MUID:93041923
A:Accession: S27200
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-389 <SAs>
A:Cross-references: GB:DI0727; NID:g220499; PIDN:BAA01570.1; PID:d1002045; PID:g2205050

Query Match 12.2%; Score 172.5; DB 2; Length 389;
Best Local Similarity 39.2%; Pred. No. 1.5e-05;
Matches 38; Conservative 4; Mismatches 20; Indels 35; Gaps 3;
OY 21 SFWAPPGIV--LPCTSYPRRQGRPPPPPPPPPLPLPPPPPPPLPLPLPLPKKGNHS 78
Db 4 SPTANGSIDSTVTVSPSPPTSGPAAPPPPPPP--PPPPPPPLPPPLPLA----- 54
OY 79 TGLCLLVFMFVVALVGLGMPQLFHLQKREPP 115
Db 55 -----SLSHCGSGQASPP 67

Search completed: April 24, 2001, 15:33:06
Job time: 97 sec

```

```

Query Match          12.2%  Score 172.5;  DB 2:  Length 389;
Best Local Similarity 39.2%  Pred. No. 1.5e-05;
Matches 38;  Conservative 4;  Mismatches 20;  Indels 35;  Gaps 3;

QY      21  SPWAPPGTV--IPCTSVPRRRGQRPPPPPPPLPLPPPPPLPLPLPKKRGNH 78
      |||||:::| | | | | ||||| | ||||| | |||||
DB      4  SPTAANGSIDSTTYVSPPPTSGPAAPPPPPPP---PPPPPPPLPLPPPLA----- 54

QY      79  TGICLLVMEFWLVALVGLGMLFOLPHLOKEPPDP 115
      || | | | | | | | | | | | | | | | | | |
DB      55  -----SLSHCGSQASPP 67

Search completed: April 24, 2001, 15:33:06
Job time: 97 sec

```

Search completed: April 24, 2001, 15:33:06  
Job time: 97 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2001, 15:33:06 ; Search time 26.96 Seconds  
(without alignments)  
706.092 Million cell updates/sec

Title: US-09-508-849-2

Perfect score: 1504  
Sequence: 1 MQQPFNYPQIYWVDSAS.....SELIVNFESQFFGLYKL 277

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR-67:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1492	99.2	281	2	Fas ligand - human
2	1127	74.9	279	2	Fas ligand - mouse
3	1107.5	73.6	278	2	Fas ligand - rat
4	208	13.8	202	1	tumor necrosis fac
5	208	13.8	202	1	tumor necrosis fac
6	195	13.0	197	1	tumor necrosis fac
7	194	12.9	205	1	tumor necrosis fac
8	187.5	12.5	232	1	lymphotoxin alpha
9	185.5	12.3	204	1	tumor necrosis fac
10	185.5	12.3	234	1	tumor necrosis fac
11	182.5	12.1	204	1	lymphotoxin - bovi
12	182	12.1	233	1	lymphotoxin - bovi
13	177	11.8	141	2	hypothetical proli
14	176	11.7	233	1	tumor necrosis fac
15	174	11.6	233	1	tumor necrosis fac
16	173	11.5	234	1	tumor necrosis fac
17	172	11.4	599	2	phosphorin-S - Vo
18	171.5	11.4	415	1	acrosin (EC 3.4.21
19	169.5	11.3	185	2	tumor necrosis fac
20	169.5	11.3	485	2	sulfated surface g
21	165.5	11.0	389	2	proline-rich prote
22	164	10.9	235	2	tumor necrosis fac
23	163.5	10.9	306	2	lymphotoxin-beta -
24	163	10.8	233	2	tumor necrosis fac
25	163	10.8	431	2	acrosin (EC 3.4.21
26	162.5	10.8	234	1	tumor necrosis fac
27	161	10.7	193	2	tumor necrosis fac
28	160.5	10.7	1206	2	formin isoform IV
29	160.5	10.7	1468	2	formin - mouse

30	159.5	10.6	421	1	acrosin (EC 3.4.21
31	159	10.6	235	1	tumor necrosis fac
32	155.5	10.3	440	2	glyceraldehyde-3-p
33	155	10.3	235	2	tumor necrosis fac
34	154.5	10.3	502	2	Wiskott-Aldrich sy
35	154.5	10.3	1110	2	hypothetical prote
36	153	10.2	760	2	extensin homolog T
37	152	10.1	487	2	nuclear protein EB
38	151	10.0	196	2	cysteine-rich exte
39	151	10.0	439	2	chitinase (EC 3.2.
40	151	10.0	980	2	regulatory protein
41	150.5	10.0	464	2	extensin - Volvox
42	150.5	10.0	1255	2	diaphanous protein
43	150	10.0	1460	1	immediate-early pr
44	149.5	9.9	645	2	hypothetical prote
45	148	9.8	1171	2	diaphanous-related

## ALIGNMENTS

RESULT 1  
138707  
Fas ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
C:Accession: J18707; J02340; S57565; I38554  
R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.  
Int. Immunol. 6, 1567-1574, 1994  
A:Title: Human Fas ligand: gene structure, chromosomal location and species specific  
A:Reference number: J18707; MUID:95127560  
A:Accession: J18707  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-281 <RES>  
A:Cross-references: EMBL:U11821; NID:9595430; PIDN:AC50124.1; PID:9595431  
R:Mita, E.; Hayashi, N.; Ito, S.; Takehara, T.; Hijioka, T.; Kashihara, A.; Fusamoto, Biochem. Biophys. Res. Commun. 204, 468-474, 1994  
A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.  
A:Reference number: J02340; MUID:95071350  
A:Accession: J02340  
A:Molecule type: DNA  
A:Residues: 1-281 <MIT>  
A:Cross-references: GB:D38122; DDBJ:D29820; NID:9601892; PIDN:BA07320.1; PID:g136990  
R:Schatzlein, C.E.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: S57565  
A:Accession: S57565  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-281 <SCH>  
A:Cross-references: EMBL:X89102; NID:9887455; PID:9887456  
R:Allderfer, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; J. Exp. Med. 181, 71-77, 1995  
A:Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.  
A:Reference number: I38554; MUID:95105731  
A:Accession: I38554  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-281 <REZ>  
A:Cross-references: EMBL:U08137; NID:9624627; PIDN:AC50071.1; PID:9624628  
C:Genetics:  
A:Gene: FasL  
A:Introns: 131/1, 116/3  
C:Keywords: glycoprotein; transmembrane protein  
F:80-102/Domain: transmembrane #status predicted <TMM>  
F:76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.2%; Score 1492; DB 2; Length 281;  
Best Local Similarity 98.6%; Pred. No. 5.3e-103;  
Matches 277; Conservative 0; Mismatches 0; Indels 4; Gaps 1;



Query Match	13.8%;	Score 208;	DB 1;	Length 202;
Best Local Similarity	32.7%;	Pred. No. 1.5e-08;		
Matches 54;	Conservative 28;	Mismatches 71;	Indels 12;	Gaps 3;
QY	123	TASSLGHSPPEPK-----ELRKVAHLTGKSNRSNRPLEWEDYIGVLLSGVYKKKGGLV	178	
	::		::	::::

```

Db      40 SASRNA--QPOKHLTHELLPKPAHLVYPSKNSLIRANTDPAFLRHGCSLNNSLL 97
Oy      179 INETGLFYFSKYVRFGSCN-----NLPLSHKVYRNRSKYRPODLVMMEGRKMSTCTTG 232
       | : |||||:::| : ||:||:   | : || : | : || : | : || : | : || : |
Db      98 IPTSGLYFYSQQVSSEGCSPRAIPPTPIYLAEHVOQLSSQYPFHVPILASNAKSYYPGIQ 157
Oy      233 QMNRASYIGAVFNLTSAHDLYVNSELVLNFEESSQTFFGLYKL 277
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      158 GPWVSMYGAVFLLSKGDQLSTHTDGISLHFSPSTVFEGAFAL 202

RESULT        6
JH0309
tumor necrosis factor beta precursor - rabbit
N.Alternate names: lymphotoxin; TNF beta
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: JH0309; PNM098
R.Shakhov, A.N.: Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A.Title: Structural analysis of the rabbit TNF locus, containing the genes encoding T
A.Reference number: JH0309; MUID:91065534
A.Accession: JH0309
A.Molecule type: DNA
A.Residues: 1-197 <SH2>
A.Cross-references: GB:M60340; GB:M35326; NID:g165754; PID:AAA31483.1; PID:g165755;
R.Shakhov, A.N.: Kuprash, D.V.; Tutetskaya, R.L.; Azizov, M.M.; Andreyeva, A.V.; Neddo
MOL. Biol. (Mosk.) 23, 1743-1750, 1989
A>Title: Cloning and structural analysis of the genes, coding for rabbit tumor necros
A.Reference number: PM098; MUID:90220566
A.Accession: PNM098
A.Molecule type: mRNA
A.Residues: 1-197 <SHA>
A.Cross-references: GX:S5745; NID:g297167; PID:CMA39275.1; PID:g297168
A.Genetics:
A.Introns: 25/3; 61/1
C.Superfamily: tumor necrosis factor
C.Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
E.1-26/Domain: signal sequence #status predicted <SIG>
F.27-197/Product: Lymphotoxin #status predicted <MAT>

Query Match          13.0%; Score 195; DB 1; Length 197;
Best Local Similarity 26.0%; Pred. No. 1.3e-07;
Matches    60; Conservative    27; Mismatches    84; Indels     60; Gaps      7;

Oy      55 PPPPPRPRLPRLPRPKKRGNHGCLLVFPNVLAVALGGMQLPHLOKEIAEL 114
       |||||         |||
Db      19 PPPPGAAGLGAAEFPPSAR-----                               38
Oy      115 RESTSQMHVASLSGHPSPEKKELRKVAHLTGSNSRMPLWE-DRYGIALLSGVKYK 173
       | : | | : | | | : | : | | : | : | : | : | : | : | : | : | : |
Db      39 -----MQQRQIKRFHGIST-----LKPAHALVDGPSAAD-SLRKANTRDALRIKGFSLS 87
Oy      174 KGVIVNETGLFYFSKYVRFGSCN-----NLPLSHKVYRNRSKYRPODLVMMEGRKMMS 227
       | : | : |||||:::| : ||:||:   | : || : | : || : | : || : |
Db      88 NNSLIYPSGGSLFYFSQVVSEGCSPKAIPPPIYLAEHVOLFSSQYSPHYPLLAAQ-KS 146
Oy      228 YCTTQG-MMARSSYLGAVPNLTSAHDLYVNSELVLNFEESSQTFFGLYKL 277
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      147 VCPGPQGPWVRSVYOGAVFLLTQGDQLSTHTDGIAMHLLSPSSVEFGAFAL 197

RESULT        7
OMNHUX
lymphotoxin alpha precursor - human
N.Alternate names: Lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
C.Species: Homo sapiens (man)
C.Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000
C.Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951; A01645;
R.Nedvin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Maylor, S.L.; Sakaguchi, A.Y.; Goedde
J. Cell. Biochem. 29, 171-181, 1985
A>Title: Structure and chromosomal localization of the human lymphotoxin gene.
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A:Reference number: A92755; MUID:86086150  
 A:Accession: A92755  
 A:Molecule type: DNA  
 A:Residues: 1-59, 'N', 61-205 <NED>  
 R:Rits, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka  
 Nature Genet. 3, 137-145, 1993  
 A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a  
 A:Reference number: S36152; MUID:93272029  
 A:Accession: S36152  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-12, 'R', 14-205 <IRI>  
 A:Cross-references: EMBL:Z15026; NID:937211; PIDN:CAA78746.1; PID:937213  
 R:Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.  
 Immunogenetics 33, 50-53, 1991  
 A:Title: Haplotypic polymorphisms of the TNF gene.  
 A:Reference number: 154482; MUID:91139175  
 A:Accession: 154482  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-124, 'P', 126-205 <RES>  
 A:Cross-references: GB:M55913; NID:9339742; PIDN:AAB59455.1; PID:9339743  
 A:Experimental source: ancestral haplotype 57.1  
 A:Note: 59-Asn was also found (ancestral haplotype 8.1)  
 R:Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringham, T.S.; Henzel, W.J.; Jarrett, J.A.;  
 Nature 312, 721-724, 1984  
 A:Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour  
 A:Reference number: A93350; MUID:85086243  
 A:Accession: A93350  
 A:Molecule type: mRNA  
 A:Residues: 1-205 <GRA>  
 A:Cross-references: GB:X01393; NID:934444; PIDN:CAA25649.1; PID:934445  
 A:Experimental source: lymphoblastoid cell line RPMI-1788  
 R:Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.A.;  
 Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986  
 A:Title: Tumor necrosis factors: gene structure and biological activities.  
 A:Reference number: A32877; MUID:87217059  
 A:Accession: B32877  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 35-205 <GDE>  
 R:Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.  
 J. Biochem. 100, 727-733, 1986  
 A:Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell hy  
 A:Reference number: A91906; MUID:87057135  
 A:Accession: A91906  
 A:Molecule type: mRNA  
 A:Residues: 1-59, 'N', 61-205 <KOB>  
 A:Cross-references: GB:D00102; NID:9219913; PIDN:BAA00064.1; PID:9219914  
 A:Note: the authors translated the codon TAT for residue 156 as Thr and ACC for residue  
 R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An  
 Lymphokine Res. 7, 175-185, 1988  
 A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and  
 A:Reference number: A61478; MUID:86501617  
 A:Accession: A61478  
 A:Molecule type: protein  
 A:Residues: 56-79, 86-95, 'X', 97, 'X', 99, 119-151, 'XX', 154-162, 'X', 164, 'X', 166, 'X', 168, 'X', 1  
 R:Voigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.  
 FEBS Lett. 314, 85-88, 1992  
 A:Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylatic  
 A:Reference number: S26951; MUID:93083656  
 A:Accession: S26951  
 A:Molecule type: protein  
 A:Residues: 35-59, 'N', 61-205 <VOI>  
 A:Note: 60-Thr was also found  
 R:Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.  
 Arch. Biochem. Biophys. 304, 144-153, 1993  
 A:Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO  
 A:Reference number: S34742; MUID:93311995  
 A:Contents: annotation  
 C:Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction,  
 while having no detrimental effect on normal cells. It can also act synergistically with

C:Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of dif  
 ferent activities but are produced by different cell types and have different induction  
 C:Genetics:  
 A:Gene: GDB:ITFA; LIT; TNFR  
 A:Cross-references: GDB:120442; OMIM:153440  
 A:Map position: 6p21.3-6p21.3  
 A:Introns: 33/3; 69/1  
 A:Note: the first intron occurs before the initiator codon  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxic; status predicted <SIS>  
 F:1-34/Domain: signal sequence  
 F:35-205/Product: lymphotoxin (status predicted <MAV>  
 F:41/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F:96/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 12.9%; Score 194; DB 1; Length 205;  
 Best Local Similarity 27.5%; Pred. No. 1.6e-07;  
 Matches 56; Conservative 34; Mismatches 90; Indels 24; Gaps 4;

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81 LCLLVFPMVLVAVGL-GIGMFPLQLKELAELESTQMTASSLGHPSPPEKKEI 139
   ||| : ||| ||| | | | | | | | | | | | | | | | | | | | |
19 LLLGLLVLPAGGLPGV-----LTPSAQTARQHPKHLAHSF-----L 61
   ||| : ||| : | | | | | | | | | | | | | | | | | | | |
140 RYVAHLTGKSNRSMLEMDTYGLVLSGVKKGLVNETGLFYVSKYFRQ--- 196
   ||| : ||| : | | | | | | | | | | | | | | | | | | | |
62 KPAHLIGPSPKNSLLMRANTRAFLQDGFSLNNSLLVPTGIVFYVSOVFSKAYS 121
   ||| : ||| : | | | | | | | | | | | | | | | | | | | |
197 ---SCNNPLPSHKVYRNRSKYPODLYMEGKMMSCYCTGOMARRSYLCAVFLTSADHL 253
   : | : | : | : | : | : | : | : | : | : | : | : | : | : |
122 PKATSSPLVLAHEVLFSSQYPPHPLSSQKVVYDGLDEPWLMSYHGAAPQLTGDDL 181
   : | : | : | : | : | : | : | : | : | : | : | : | : | : |
254 YVAVSELVNFESOTFFGLYKL 277
   : | : | : | | | | | | | | | | | | | | | | | | | |
182 STHTDGIPIHVLSPSTVFPGAFAL 205
   : | : | : | | | | | | | | | | | | | | | | | | | |

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RESULT 8  
 S12606  
 tumor necrosis factor alpha precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #tex\_change 04-Feb-2000  
 C:Accession: S12606; S17290; S18965; 146659  
 R:Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.  
 Nucleic Acids Res. 18, 5564, 1990  
 A:Title: Gene sequence of porcine tumor necrosis factor alpha.  
 A:Reference number: S12606; MUID:91016861  
 A:Accession: S12606  
 A:Molecule type: DNA  
 A:Residues: 1-232 <DRE>  
 A:Cross-references: EMBL:X54001; NID:92135; PIDN:CAA37949.1; PID:92136  
 R:Kuhert, P.; Muehrich, C.; Peterhans, E.; Pauli, U.  
 Gene 102, 171-178, 1991  
 A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a  
 A:Reference number: S17289; MUID:91340150  
 A:Accession: S17290  
 A:Molecule type: DNA  
 A:Residues: 1-232 <KUB>  
 A:Cross-references: EMBL:X54859; NID:92132; PIDN:CAA38639.1; PID:92134  
 A:Note: the authors translated the codon GAG for residue 202 as Gly  
 R:Choi, C.S.; Mollitor, T.W.; Lin, G.F.; Murlaugh, M.P.  
 submitted to the EMBL Data Library, January 1991  
 A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis  
 A:Reference number: S18965  
 A:Accession: S18965  
 A:Molecule type: mRNA  
 A:Residues: 1-232 <CHO>  
 A:Cross-references: EMBL:X57321; NID:92137; PIDN:CAA40591.1; PID:92138  
 R:Pauli, U.; Beutler, B.; Peterhans, E.  
 Gene 81, 185-191, 1989  
 A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain react  
 A:Reference number: 146659; MUID:90034181  
 A:Accession: 146659

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A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 44-232 <PAU>
A:Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C:Genetics:
A:Introns: 62/3; 78/1; 93/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myr
F:1-77/Domain: propeptide #status predicted <Pro>
F:78-232/Product: tumor necrosis factor alpha #status predicted <Mat>
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
E:81/Binding site: carbohydrate (ser) (covalent) #status predicted
F:144-176/Disulfide bonds: #status predicted

Query Match          12.5%; Score 187.5; DB 1; Length 232;
Best Local Similarity 29.2%; Pred. No. 5.7e-07;
Matches    68; Conservative   26; Mismatches   92; Indels   47; Gaps   10;

      72 KKRGRHSVGLCLLVNFNVLAVALYGLGMPLDHL-----QKE-----LAEIR 115
Db       20 RAGGPGGSRRRCICLSLFSEFL--LVAGAATTLFCLLHFEYIGIPQKEEFPAPGISINPDLGG 177
Oy     116 ESTSOMHTASSLGHSPPEKKELRKVAHLTGCKNSRSMPLMEPTGYGLVL-SGVTKRK 174
            |||           |||||         |::|        |::|
Db       78 RSSQSOTSD-----KPVAHVANVAABEQ-LDMQGCIYNALLANKSVKLKD 120
Oy     175 GGLVINETGLFYVSKEYFRGSC---NNLPISHKYVMNRSKYPDDLVMMEGRMSYC--- 229
            |||           |||||         |::|        |::|
Db     121 NLQIVPTDGILYLITYSQVFLEFGCGCPSTNVFLHTISRIAVSY-QTRKNVLSAIRKPCQRE 179
Oy     230 ----TTGQMAMASSYLGAVENLTSDHLTVNASELSLVNFES-OTFEGIKYL 277
Db     180 TPEGAAEKRPWEPIYILGCVFOLEKDDRLSAEIPLDPVIDFAESGCVVYGIAL 232

RESULT      9
S17289
tumor necrosis factor beta precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S17289
R:Kuhnert, P.; Wuehlrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
AtTitle: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A:Reference number: S17289; MUID:91340150
A:Accession: S17289
A:Molecule type: DNA
A:Idues: 1'204 <KHU>
A:Cross-references: EMBL:X54859; NID:g21132; PIDN:CAA38638.1; PID:g21133
C:Genetics:
A:Introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F:1-33/Domain: signal sequence #status predicted <Sig>
F:34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match          12.3%; Score 185.5; DB 1; Length 204;
Best Local Similarity 29.0%; Pred. No. 6.9e-07;
Matches    62; Conservative   28; Mismatches   87; Indels   37; Gaps   8;

      78 STGCLLVNFVFWL----VALVGILGIMFQLRHLOKETALDELSTOSMHTASSLGHPSPP 133
Db     14 STPIILLGLLALAPEAQGLRGVGI-----PPSAQAQRPHQHNP 52
Oy    134 PE--KKELRKVAHLTGCKNSRSMPLEWE-DIYGIYLLSGVKRYKKGGLVINETGLFYYSK 190
            |::|           |||||         |::|        |::|
Db     53 KHIAQTTPKAHLVDGPSTPD-SLRMRANTDRAFLRHGFTLLSNSNLVPITSGIFYVSQQ 111
Oy    191 VYFRQSC-----NNLPISHKYVMNRSKYPDDLVMMEGRMSYSTCTGQ-MMARSSYLGA 243
            |||           |||||         |::|        |::|
Db     112 IVVEGSGCCPRKAPPPLLYAHAEVOLFFSSQYPRHHVILLSAO-KSVCPGPGGPMWVASVYGOA 170

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Ox      244  VENTLSADHLVWVNSSELSLVNFEESQTEFGYKLL 277
          || || | | : | ||| : |
Db      171  VFLITGGDGLSTHTDGTDPHLLSPSSVEFGAPAL 204

RESULT  10

J01344
tumor necrosis factor alpha precursor - horse
N:Alternate names: cachectin; TNF alpha
C:Species: Equus caballus (domestic horse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: J01344
R:Su. X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis
A:Reference number: J01344; MUID:92084125
A:Accession: J01344
A:Molecule type: DNA
A:Residues: 1-234 <SUX>
A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C:Comment: This protein is an important proximal mediator of endotoxemia.
C:Genetics:
A:Gene: TNF-alpha
A:Introns: 62/3; 79/1; 95/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; n
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F:19-20/Binding site: myristate (Lys) (covalent) #status predicted
F:82/Binding site: carboxylate (Ser) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

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Query Match 12.3%; Score 185.5; DB 1; Length 234;
Best Local Similarity 27.7%; Pred. No. 8.1e-07;
Matches 62; Conservative 36; Mismatches 99; Indels 27; Gaps 10;

QY      72  KKRGNHSTGLCLLVNFFMVALVGLGMEFLHL-----QKELARESTSQMHTA 124
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      20  KAGGQGSRRCLCLSLFSL--LVAGATTLFCLLHFVIGVPGREQDLRPAQSINPL--A 75
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      125  SLLGHPSPPEPPEKKELRKVAHLTGKNSRSMPLF--EDTIYGLVLSGVYKKKGVLINETG 183
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      76  QTLRSSRTPSPDK--PVAHVAVNPADEGQ--LQWLSGRANALLANGVKLTDMQVVPIDG 131
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      184  LYFVYSKYVFRGQSC--NNLPLSHKYVMKNSKYPODVLVMECKKMSYCTT-----GQM 234
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      132  LYLLISQVLEKQGGCPSTHVLPLHTIRLANSYPSKVNLLSA--IKSPCHTESPEQAEAKP 190
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      235  WARSSYLGAVFNLTSADHLVYNVSESLVNFEE--QTEFGLYKL 277
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      191  WPEPIYLGVPFLERKGDQLSAEINQPNYLDFAESQGVYFGIALL 234
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
S24641
Lymphotoxin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I46046; S24641
R:Clusts: 1; Cleuter: Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A:Title: Cloning and characterization of the tandemly arranged bovine Lymphotoxin and
A:Reference number: I46046; MUID:94083525
A:Accession: I46046
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-204 <CLD>
A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797
C:Genetics:
A:Introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor

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A:Reference number: A61478; MUID:88301617  
 A:Accession: B61478  
 A:Molecule type: protein  
 A:Residues: 83-102:109-119:121-128,'X',130-131:142-144,'X',146,'XXX',150-152:159-174:180  
 R:Marmout, A.; Fransen, L.; Tavenier, J.; Van Der Heyden, J.; Tilard, R.; Kawashima, Eur. J. Biochem. 152, 515-522, 1985  
 A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison  
 A:Reference number: 153311; MUID:86030296  
 A:Accession: 153311  
 A>Status: translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-233 <MAR>  
 A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
 A:Experimental source: U-937 cells  
 R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M. Eur. J. Biochem. 235, 431-437, 1996  
 A:Title: O-GlcNAcylated species of natural human tumor necrosis factor-alpha.  
 A:Reference number: 562610; MUID:96202967  
 A:Accession: 562610  
 A:Molecule type: protein  
 A:Residues: 77-99 <TRAK>  
 R:D'Alfonso, S.; Richardt, P.M. Immunogenetics 39, 150-154, 1994  
 A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region  
 A:Reference number: 154522; MUID:94102809  
 A:Accession: 154522  
 A>Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <DAL>  
 A:Cross-references: GB:S68530; NID:g544751  
 R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H. J. Exp. Med. 176, 1053-1062, 1992  
 A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys  
 A:Reference number: A59163; MUID:93018820  
 A:Contents: annotation; Identification of myristylated lysines  
 R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Motilal, B.; Spencer, S.A.; Henzel, W.J.; Bring J. Biol. Chem. 260, 2345-2354, 1985  
 A:Title: Human tumor necrosis factor. Production, purification, and characterization.  
 A:Reference number: A92511; MUID:85130974  
 A:Contents: annotation; disulfide bond  
 C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction out detriment to normal cells. It can also act synergistically with interferon gamma to C:Comment: TNF-alpha and -beta (lymphokine) are the products of different genes closely ut are produced by different cell types and have different induction kinetics.  
 C:Genetics:  
 A:Gene: GDB:TNF; TNFA  
 A:Cross-references: GDB:120441; OMTM:191160  
 A:Position: 6p21.3-6p21.3  
 A:Residues: 62/3; 78/1; 94/1  
 C:Complex: homotrimer  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: cytokine; cytotoxic; glycoprotein; homotrimer; lipoprotein; lymphokine; mact F:1-76/Domain: propeptide #status predicted <PRO>  
 F:77-233/Product: tumor necrosis factor #status experimental <MAR>  
 F:19,20/Binding site: myristate (lys) (covalent) #status experimental  
 F:81/Binding site: carbonylate (Ser) (covalent) (partial) #status experimental  
 F:145-177/Disulfide bonds: #status experimental

Query Match 11.7%; Score 176; DB 1; Length 233;  
 Best Local Similarity 27.2%; Pred. No. 4e-06;  
 Matches 64; Conservative 32; Mismatches 93; Indels 46; Gaps 11;

QY 70 PLKRGHSTGICLVMEFVNLVALVGLGFMFHL-----OKE-----LAE 113  
 DB 18 PKKTGGPGSRCLPLSFLSFL--VAGATVLFCLHFGVIGPQREPPKPSLISPLAQ 75  
 QY 114 LRETSQMHHTASSLGHPPPEPEKELRKVAHLTGKSNRSRSMPLMEDTYGYLL-SGVKY 172  
 DB 76 AVRSSRT-----PSDKP-----VAHVANPQAEQO-LQWLNRRANALLANGVEL 119  
 QY 173 KKGGLVNETGLYFYYSKYVFRGSC--NNLPLSHKRYVMRNSKYPQDILVMEGKMSYC- 229

DB 120 RDNOLVSEGLIYLYISVLFKGGCPSFHWLHTHTISRIAVSY-QTKVNLISAIRKSPQ 178  
 QY 220 -----TTGQWARRSSYLGAVENTLSADHLVYNVSELSVNEEES-QTFEGLYKL 277  
 DB 179 RETPGAEAKPWEPIYILGAVFQLEKGRLSAEIRPDIIDPAESGQYFGIIAL 233

# RESULT 15 S22052

tumor necrosis factor alpha precursor - baboon  
 C:Species: Papio sp. (baboon)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text-change 04-Feb-2000  
 C:Accession: S22052  
 R:Sanjanwala, M.; Edwards, A. submitted to the EMBL Data Library, September 1991  
 A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.  
 A:Reference number: S22052  
 A:Accession: S22052  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-233 <SAM>  
 A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160  
 C:Genetics:  
 A:Introns: 62/3; 78/1; 94/1  
 C:Superfamily: tumor necrosis factor  
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
 F:19,20/Binding site: myristate (lys) (covalent) #status predicted  
 F:81/Binding site: carbonylate (Ser) (covalent) #status predicted  
 F:145-177/Disulfide bonds: #status predicted

Query Match 11.6%; Score 174; DB 1; Length 233;  
 Best Local Similarity 27.7%; Pred. No. 5.7e-06;  
 Matches 65; Conservative 31; Mismatches 93; Indels 46; Gaps 11;

QY 70 PLKRGHSTGICLVMEFVNLVALVGLGFMFHL-----OKE-----LAE 113  
 DB 18 PKKTGGPGSRCLPLSFLSFL--LVAGATVLFCLHFGVIGPQREPPKPSLISPLAQ 75  
 QY 114 LRETSQMHHTASSLGHPPPEPEKELRKVAHLTGKSNRSRSMPLMEDTYGYLL-SGVKY 172  
 DB 76 AVRSSRT-----PSDKP-----VAHVANPQAEQO-LQWLNRRANALLANGVEL 119  
 QY 173 KKGGLVNETGLYFYYSKYVFRGSC--NNLPLSHKRYVMRNSKYPQDILVMEGKMSYC- 229  
 DB 120 RDNOLVSEGLIYLYISVLFKGGCPSFHWLHTHTISRIAVSY-QTKVNLISAIRKSPQ 178  
 QY 230 -----TTGQWARRSSYLGAVENTLSADHLVYNVSELSVNEEES-QTFEGLYKL 277  
 DB 179 RETPGAEAKPWEPIYILGAVFQLEKGRLSAEIRPDIIDPAESGQYFGIIAL 233

Search completed: April 24, 2001, 15:33:07  
 Job time: 98 sec

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|||||
51 CAGTGGCAGCTCTCCCTGGGCCCCCTCCAGGACAGATTCTTCCTGTCCAA 100
34 htservalProArGArgProGlyGlnArgArgProProProProPro 50
101 CCTGTGTGCCCAAGAGCCCTGGTCAAGAGGAGGCCACACACAGCCGCCA 150
51 ProProProLeuProProProProProProProProLeuProProLeuPr 67
151 CCGCCACACACTACCTCCGCGCGCCGCGCCACCACTGCTCCACTACC 200
67 oleuProProLeuLysArgGlyGlnHisSerThrGlyLeuCysLeuL 84
201 GGTGGCAGCCCTGAGAGAGAGAGAGAACACACAGCAGAGCCCTGTCTCC 250
84 euvalMetPheMetValLeuValAlaLeuValGlyLeuGly 100
251 TGTGTAGTGTTCATGCTTCTGTGCTGCTGCTGATGAGATTGGGCTGGG 300
101 MetPheGlnLeuPheHisLeuGlnLysGlu..... 110
101 ATGTTTCAGCTTTCACCTACAGAGAGAGCTGGCAGAACTCCGAGAGTC 350
111 ..... P 111
351 TACACAGCCAGATGCACAGACATCATCTTTGAGAAACAAATAGGCCACC 400
111 roserProProGlyLysLysGlyLeuArgLysValAlaHisLeuThr 127
401 CCGTGCACCCCTCGAAAAAGAGAGCTAGAGAAAGTGGCCCTTTAAACA 450
128 GlyLysSerAsnSerArgSerMetProLeuGluTrpGluAspThrTyrG 144
451 GGCAGACTCAACACTCAAGTCCATCTGGAATGGGAAGACACCTATGG 500
144 yileValleuLeuSerGlyValLysTyrLysLysGlyLeuValIle 161
501 AATTGTCCTGCTTCTGAGTGAATRAAGAGGGGCTGTGTATCA 550
161 snGluThrGlyLeuTyrPheValTyrSerLysValTyrPheArgGlyGln 177
551 ATGAACTGGGCTGTACTTGTATATCCAAAGTATACTTCGGGGTCACA 600
178 SerCysAsnAsnLeuProLeuSerHisLysValTyrMetArgAsnSerly 194
601 TCTTGGCAACACTGCTCCCTGAGCCACAAAGTCTACATGAGAACTCTAA 650
194 sTyrProGlnAspLeuValMetMetGluGlyLysMetMetSerTyrCysT 211
151 GATGCCCAAGATCTGTGATGATGAGAGGGAGATGATGAGCTACTGCA 700
211 hTThrGlyGlnMetTrpAlaArgSerSerTyrLeuGlyAlaValPheAsn 227
701 CTACTGGGAGATGGGCCCGCAGAGCTACTGGGGGAGTTCAT 750
228 LeuThrSerAlaAspHisLeuTyrValAsnValSerGluLeuSerLeuVa 244
751 CTTACAGTGGCTGATCATTTATATGCAACGATATGAGCTCTCTCTGGT 800
244 lasnPhenGluLeuSerGlnThrPhePheGlyLeuTyrLysLeu 258
801 CAATTTTGAGGAATCTCAGACGTTTTCGGCTTATATTAAGCTC 843
seq_name: /cgn2_6/ptodate/2/lna/5B_COMB.seq:US-08-810-453-1
seq_documentation_block:
: Sequence 1, Application US/08810453
: Patient No. 5858990
: GENERAL INFORMATION:
: APPLICANT: Walsh, Kenneth
: TITLE OF INVENTION: FAS LIGAND COMPOSITIONS FOR TREATMENT OF
: PROLIFERATIVE DISORDERS
: NUMBER OF SEQUENCES: 2

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CORRESPONDENCE ADDRESS:
ADDRESS: Wolf, Greenfield & Sacks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,453
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: S1237/7004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
TELEX: 343
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1790 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 86..931
FEATURE:
NAME/KEY: "transmembrane domain, amino acids 81-102"
LOCATION: 326..391
FEATURE:
NAME/KEY: "potential N-linked glycosylation site, amino acid 184"
LOCATION: 635..637
FEATURE:
NAME/KEY: "potential N-linked glycosylation site, amino acid 250"
LOCATION: 833..835
FEATURE:
NAME/KEY: "potential N-linked glycosylation site, amino acid 260"
LOCATION: 863..865
US-08-810-453-1
alignment_scores:
Quality: 1389.50 Length: 281
Ratio: 5.386 Gaps: 1
Percent Similarity: 91.815 Percent Identity: 91.815
alignment_block:
US-09-508-849-1 x US-08-810-453-1 ..
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17 rserAlaSerSerProTrpAlaProProGlyThrValLeuProCysProT 34
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136 CAGTGCACCTCTCCCTGGGCCCCCTCCAGGACAGTTCCTCCGTCCAA 185
34 htservalProArGArgProGlyGlnArgArgProProProProPro 50
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186 CCTGTGTGCCAGAGGCGCTGTCAAGAGGCGCACACACACCGGCA 235
51 ProProProLeuProProProProProProProLeuProLeuPr 67
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236 CCGCCACACACACACACCTCCGCGCGCGCGCACACACCTCCACTACC 285
67 OLeuProProLeuLysLysArgGlyAsnHisSerThrGlyLeuLysLeuL 84
GCTGCCACCGCTGAGAGAGAGAGAGACACACAGCAGCGCTGTGTCTCC 335
286 GCTGCCACCGCTGAGAGAGAGAGAGACACACAGCAGCGCTGTGTCTCC 335
84 euValMetPhePheMetValLeuValAlaLeuValGlyLeuGlyLeuGly 100
|||||
336 TTGTGATGTTTTTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 385
101 MetPheGlnLeuPheHisLeuGlnLysGlu..... 110
386 ATGTTTCAGCTCTTCCACCTACAGAGAGAGCTGGCAGAACTCCGAGAGTC 435
111 .....P 111
436 TACCAAGCCAGATGCACACAGCATCTTTGGAGAGAAATAGGCCAC 485
111 roSerProProProGluLysLysGluLeuValAlaHisLeuThr 127
|||||
486 CCAGTCCACCGCTGAAAAAGAGAGCTGAGAGAAAGTGGCCCATTTACA 535
128 GlyLysSerAsnSerArgSerMetProLeuGluTrpGluAspThrTyrG 144
|||||
536 GGCAAGTCCACACTCAAGTCCAGTCTCTGAGATGGAGAGACACTATGG 585
144 YLeuValLeuLeuSerGlyValLysTyrLysLysGlyLeuValIle 161
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586 AATGTCTCGCTTCTGAGAGTGAATATAAGAGGTGGCTTGATCA 635
161 snGluThrGlyLeuThrPheValTyrSerLysValTyrPheArgGlyGln 177
636 ATGAAGCTGGGCTGTACTTGTATATCCAAAGTACTTCCGGGGTCA 685
178 SerCysAsnAsnLeuProLeuSerHisLysValTyrMetArgAsnSerL 194
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686 TCTTGCAACACCTGCCCTGAGCCACAGAGCTCTACATGAGGAACTCTA 735
194 sTyrProGlnAspLeuValMetMetGluGlyLysMetMetSerTyrCys 211
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736 GTATCCACAGATCTGATGATGATGAGGAGGAGATGATGAGCTACTGCA 785
211 hrThrGlyGlnMetTrpAlaArgSerSerTyrLeuGlyAlaValAlaPhe 227
786 CTACTGGGACAGATGGGCGCGCACAGCTACTGGGGGAGCTTTCAT 835
228 LeuThrSerAlaAspHisLeuTyrValAsnValSerGluLeuSerLeuVal 244
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836 CTTACCACTGCTGATCATTTATATGTCAACGATATGTAGCTCTCTGTGT 885
244 LAspPheGlnLysSerGlnThrPhePheGlyLeuTyrLysLeu 258
886 CAATTTGAGGAATCTCAAGCTTTTGGCTTATATAAGCTC 928
seq_name: /cgn2.6/prodata/2/lna/PCTUS_COMB.seq:PCT-US95-00362-1
seq_documentation_block:
; Sequence 1, Application PC/TUS9500362
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; TITLE OF INVENTION: Ligand That Binds Fas Antigen
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00362
; FILING DATE: 06-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,138
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,559
; FILING DATE: 01-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2805-WO
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93..938
; PCT-US95-00362-1

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alignment_scores:
    Quality: 1389.50      Length: 281
    Ratio: 5.386          Gaps: 1
    Percent similarity: 91.815    Percent identity: 91.815

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alignment block:

US-09-508-849-1 x PCT-US95-00362-1 ..

Align seg 1/1 to: PCT-US95-00362-1 from: 1 to: 1841

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17 rSerAlaSerSerProTrpAlaProProGlyThrValLeuProCysPro 34
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143 CAGTGGCACCTCTCCCTGGGCGCCCTCCAGGACAGATTTCTTCCCTGCCA 192
34 hrSerValProArgArgProGlyGlnArgArgProProProProPro 50
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193 CCTGTGTGCCAGAGGCGCTGTCAAGAGAGGCGCACACACACCGGCA 242
51 ProProProProLeuProProProProProProProProProLeuPr 67
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243 CCGCCACACACACACCTCCGCGCGCGCGCCACACCACTGCTCCACTACC 292
67 OLeuProProLeuLysLysArgGlyAsnHisSerThrGlyLeuLysLeuL 84
GCTGCCACCGCTGAGAGAGAGAGAGACACACAGCAGCGCTGTGTCTCC 342
293 GCTGCCACCGCTGAGAGAGAGAGAGACACACAGCAGCGCTGTGTCTCC 342
84 euValMetPhePheMetValLeuValAlaLeuValGlyLeuGlyLeuGly 100
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343 TTGTGATGTTTTTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 392
101 MetPheGlnLeuPheHisLeuGlnLysGlu..... 110
393 ATGTTTCAGCTCTTCCACCTACAGAGAGAGCTGGCAGAACTCCGAGAGTC 442
111 .....P 111
443 TACCAAGCCAGATGCACACAGCATCTTTGGAGAGAAATAGGCCAC 492

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111	roserioPProProGluLysLysGluLeuAlaArgLysValAlaHisLeuThr	127
493	CCAGTCACCCCTGGAAAAAAGAGGCTGAGGAAGTGGCCATTATACA	512
128	GlyLysSerAsnSerArgSerMetProLeuGluIuTrpGluAspThrTyrGlu	144
543	GCCAAATGCCAACCAACAGAGCTCCATGCCCTGGCAATGGGAACACCCATTATGC	592
144	YIIValIleuLeuSerGluValLysTyrLysLysGluGlyIleuValIleu	161
593	AATTGTCCTGCTTTCTGGAGTAAAGTATTAAGAAGGATGGCCCTTGATCA	642
161	snGluThrGlyLeuTyrPheValTyrSerLysValTyrPheArgGlyGln	177
643	ATGAACCTGGGGCTGTCCTTGTATTTCCAAAGATATACCTCCGGGGTCAA	692
178	SerCysAsnAsnLeuProLeuSerHisLysValTyrMetArgAsnSerLys	194
693	TCCTTGACACACCTGCCCTTGAGCCACCAAGGCTATCAATGAGAACTGTAA	742
94	sTyrProGlnAspLeuValIleMetGluGluLysMetMetSerTyrCysT	211
743	GTAATCCCGAGGATCTGGTATGATGAGGAGGGAAGATGATGATGATGCA	792
211	hrThrGlyGlnMetTrpAlaArgSerSerTyrLeuGlyAlaValPheAsn	227
793	CTACCTGGGCGAGATGGGCCGCCACACCTACCTGGGGGCGAGTTTCAAT	842
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843	CTTACCAAGTGCATCATTTATATGTCAACGATCTGAGCTCTCTCGGT	892
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seq\_documentation\_block:

Sequence 4, Application PC/TUS9500362  
GENERAL INFORMATION:  
APPLICANT: IMMUNEX CORPORATION  
TITLE OF INVENTION: Ligand That Binds Fas Antigen  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/00362  
FILING DATE: 06-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/179,138  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/190,559  
FILING DATE: 01-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2805-WO  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1171 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31..870  
US95-00362-4

alignment\_scores:

Quality: 1053.50 Length: 281  
Ratio: 4.561 Gaps: 3  
Percent Similarity: 82.206 Percent Identity: 71.174

alignment\_block:

US-09-508-849-1 x PCT-US95-00362-4

Align seg 1/1 to: PCT-US95-00362-4 from: 1 to: 1171

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81 CAGTGCACCTTCATCTTGGGCTCTCCAGAGGTCAGTTTCCCTGCCAT 130
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67 oleuProProleuLysLysArgGlyAsnHisSerThrGlyLeuLysLeu 84
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228 ACTGACCCCTCTTAAGAGAAG...GACACACAACAATACTGTGTGCTTAC 274
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84 euValMetPhePheMetValLeuValAlaLeuValGlyLeuGlyLeu 100
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101 MetPheGlnLeuPheHisLeuGlnLysGlu..... 110
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325 ATGTATCAGCTCTTCACCTGCAGAGAACTGCCAGAACTCCGTGATG 374
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111 .....P 111
375 CACCAACAAGCCTTAAGATCATCTTTGAAAAACAATAGCCAC 424
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425 CCAGTACACCTCTGAAAAAAGAGCCGAGGTGTGTGTGTGTGTGTGTGT 474
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128 GlyLysSerAsnSerArgSerMetProLeuGluTrpGluAspThrTyrGl 144
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625 TCTTGCACACAGCCCTTAACACAGAGCTATATGAGAACTTAA 674
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seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: US-08-751-512-7

seq\_documentation\_block:

Sequence 7, Application US/08751512  
Patent No. 6001962  
GENERAL INFORMATION:  
APPLICANT: Ramer, J. Kevin  
APPLICANT: Williams, Lewis T.  
TITLE OF INVENTION: Modified Fas Ligands  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/751,512  
 FILING DATE: 15-NOV-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Murphy, Matthew B.  
 REGISTRATION NUMBER: 39,787  
 REFERENCE/DOCKET NUMBER: 02307K-0710005  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-576-0200  
 TELEFAX: 415-576-0300  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1131 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1128  
 OS-08-751-512-7

alignment\_scores:

Quality:	833.50	Length:	330
Ratio:	4.168	Gaps:	10
Percent Similarity:	60.606	Percent Identity:	56.970

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alignment_block:
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US-09-508-849-1 x US-08-751-512-7

Align seg 1/1 to: US-08-751-512-7 from: 1 to: 1131

[illegible]

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113  oPpPpRoglLylsYslGluLeuAtglYsValAlahlsLeuThrGlYlys 130
113  |||||
693  ACCCCCTGAAAAAGAGAGCTGAGCAAAAGTGCCCATTTAACAGCCAACT 742
130  eRAsnSerArgSerMetProLeuGluTrpGluAspThrTyGrlYlileVal 146
743  CCACATCTAAGGTCCATGCTCTTGGATATGGGAAGACCATATGCAATTGTC 792
147  LeuLeuSerGlyValLysTyTrLYsLysGlyLeuValIleAsnGluTh 163
793  CTGCTTCTTGAGAGTAGATAAAGAGGAGTGCCCTTGATGATCAATGAAC 842
163  rGlyLeuTyTrPheValTyTrSerLYsValTyTrPheArgGlyGlnSerCys 180
843  TGGCGCTGTACTTTGTATATTCAAAGATTAATCTCCGGGGTCATCTGCA 892
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893  ACAACCTGCCCTTGAGCCACACAGGCTCTACATGAGAACTCTAAGATGCC 942
197  GluAspLeuValMetMetGluGlyLYsMetMetSerTyCysThrThrGl 213
943  CAGAGATCTGATGATGAGTAGAGGGAAGATGATGAGCTACTGCATCACTGG 992
213  yGlnMetTrpAlaArgSerSerTyTrLeuGlyAlaValPheAsnLeuThS 230
993  GCAGATCTGGGCGCGACGACCTACTGGGGGCACTGTTCAATCTTACCA 104
230  eRlAAspHisLeuTyTrValAsnValSerGluLeuSerLeuValAsnPh 246
1043  GTCTGATCTATTATATGCTCAAGCTATGACCTGTGCTGTGCTCAATTTT 109
247  GluGluSerGlnThrPheGlyLeuTyTrLYsLeu 258
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seq_name: /cgn2.6/ptodate/2/lna/6A_COMB.seq:US-08-815-190A-15
seq_documentation_block:
  Sequence 15, Application US/08815190A
  Patent No. 6046310
  GENERAL INFORMATION:
    APPLICANT: Queen, Cary L.
    APPLICANT: Schneider, William P.
    APPLICANT: Vasquez, Maximiliano
    TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
    TITLE OF INVENTION: Uses
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESSES:
      ADDRESSEE: Townsend and Townsend and Crew LLP
      STREET: Two Embarcadero Center, Eighth Floor
      CITY: San Francisco
      STATE: California
      COUNTRY: USA
      ZIP: 94111-3834
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/815,190A
        FILING DATE: 11-MAR-1997
        CLASSIFICATION: 536

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25 oProGlyThrValLeuProCysPro...ThisSerValProArgArgProG 41
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APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MDAIC
FEATURE:
NAME/KEY: CDS
LOCATION: 47..919
PCT-US96-10895-5

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Quality: 187.00      Length: 180
Ratio: 1.748         Gaps: 8
Percent Similarity: 59.444      Percent Identity: 29.444

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alignment\_block:

US-09-508-849-1 x PCT-US96-10895-5 ..

Align seg 1/1 to: PCT-US96-10895-5 from: 1 to: 1366

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164 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 180
593 GAGGCGCTTATTACATCTATTCCCAACATCTCCATTCCAGAGAAC 642
179 sAsnAsnLeu.....ProL 184
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244 ValAsnPheGluGlySerGlnThrPhePheGlyLeuTyr 256
872 ATGACCTGTGATCACAAGACCACTTCTTGGAGCCTTT 910

seq_name: /cgn2_6/plodata/2/ina/6A_COMB.seq:US-08-996-139-12
seq_documentation_block:
Sequence 12, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A

```

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)233-0644  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 954 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 CLONE: hURANKL (full length)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..951  
 US-09-996-139-12

alignment\_scores:  
 Quality: 185.00 Length: 342  
 Ratio: 1.284 Gaps: 14  
 Percent Similarity: 41.813 Percent Identity: 22.515

alignment\_block:  
 US-09-508-849-1 x US-09-996-139-12 ..

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24  AAlpProGlyThrValLeuProCysProThSerValProArgArg.P 40
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5  GCGCGCCGACAGAGACTACACCA...AGTACCCTGCGTGGCTGGAGAG 51
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40  roGlyGlnArgProProProProProProProProProProPro 56
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52  ATGGG...CGCGCGCCCGGAGCCCGCCGACGAGGGCCCTCGACGCC 98
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56  oProProProProProProProProProProProProProLeuLys 73
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99  GCGCGCGCGTGGCGCGCCGACGCCGCC... 126
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73  ysArgGlyAsnHisSerThrGlyLeuCysLeuValMetPhePheMet 89
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
127  ..GCCGCTCCCGCTCC... 141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
90  ValLeuValAlaLeuValGlyLeuGlyLeuGly... 100
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142  ATGTGCTGGCCCTCCTCGTGGGCTGGGCTGGCCAGGTGTCTGCAGCGT 191
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101  ...MetPheGlnLeuPheHisLeuGlnLysGluProSerProProPro 116
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192  CGCGCTGTCTTCTATTTCAGAGCGAGATGATCCCAATAGAAATATCAG 241
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116  Lu... 116
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242  AGATGGCACTCACTGATTTATAGAAATTTGAGACTCCATGAATAATGCA 291
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116  .. 116
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292  GATTTTCAGACACAACTCTGGAGAGTCAAGATACAAATTAATACCTGA 341
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117  .. 117
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342  TTCATGTAGAGAAATTAACAGGCCCTTTCAGAGAGCTGTCAAAAGGAAT 391
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120  euArgLysVal... 123
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392  TACAAATATATCGTTGGATCAGACACATCAGAGCAGAAAGGATGTG 441
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123  ..... 123
442  GATGGCTCATGCTTAGATCTGCCAAGAGGACCAAGCTGAAGCTCAGCC 491
124  ....AlaHisLeuThrcGlyLysSerAsnSerArgSerMetPro..... 136
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492  TTTTGGCTCATCTACT.....ATTATGCCACCGACATCCATCTGTT 535
137  .....LeuGluTrpGlnAspThrTrpGlyIleValLeu 147
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536  CCCATAAGTAGAGTCTGCTCTGTTGACCATGATGCGGTGGGCCAAG 585
148  LeuSerGlyValLysTrpLysGlyGlyLeuValIleAsnGluTrpG 164
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586  ATCTCCACATGACTTTAGCAATGGAACCTAATAGTTATCAGATGG 635
164  yLeuTrpPheValTrpSerLysValTrpPheArgGlyGlnSerCysAsn 181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
636  CTTTATTACCTGATGCAACATTTGCTTTCGACATCATGAATACTTACG 685
181  sn.....LeuProLeuSerHisLysValTyrMetArg 191
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686  GAGACCTAGCTACAGAGTATCTCAACTAATGGTACGTACACTAAACC 725
192  AsnSerLysTrpProGlnAspLeuValMetMetGluGlyLysMetLse 208
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736  AGCATCAAAATCCCAAGTTCTCATACCTGATGAAAGAGAACACCA 785
208  rTyrcysThrThrGlyGlnMetTrpAlaArgSer..... 220
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786  GTAT.....TGTCAGGGAATTCGAATTCATTTT 817
221  .....TyrLeuGlyAlaValPheAsnLeuThrSerAlaAspHisLeu 234
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818  ATTCATAAACGTTGGGATTTTAAATTACGTCGTGAGAGGAATC 867
235  TyrValAsnValSerGluLeuSerLeuValAsnPheGlnGlnSerGln 251
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868  AGCATGAGGTCTCCAAACCCCTTACTGTGATCCGATCAGATGAGATGAC 917
251  rPhePheGlyLeuTyrLysLeu 258
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918  ATACTTTGGGCTTTAAAGTT 939
seq_name: /cgn2.6/ptdata/2/1na/6B_COMB.seq:US-07-705-490-1
seq_documentation_block:
: Sequence 1, Application US/07705490
: Patent No. 6107025
: GENERAL INFORMATION:
: APPLICANT: Caskey, C. T.
: APPLICANT: Nelson, David L.
: APPLICANT: Pieretti, Maura
: APPLICANT: Warren, Stephen T.
: APPLICANT: Oostre, Ben A.
: TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Thomas D. Paul
: STREET: 1301 McKinney, Suite 5100
: CITY: Houston
: STATE: Texas
: COUNTRY: U.S.A.
: ZIP: 77010-3095
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/705,490
: FILING DATE: 19910708
: CLASSIFICATION: 435

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Page 13

STATE: Tex

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2  GlnGlnProPheAsnTyrProGlyProGlnIleTyrTrpValaLapserse 18
   :::::||||:||||:|
265  GAACATCTCTTAAATAATGCGCTTGTAGAAAAGCGCCATTG6.....AGCC 222
18  rAlaSerseProTrpAlaProProGlyThyValLeuProCys..ProThr 34
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221  CGCACTTCCACACCAAGCTCTTCATCTTCTTTCAGCCCTGCTAGGCC 172
35  ...SerValProArgArgProGlyGlnArgy..... 44
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171  GGGAGCGCGCGCCCGGAGAGGTGGGTGGGGGGCGTCGAGGCCAGCGCC 122
45  ....ProProProProProProProProProProProProProProPro 60
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121  GCGCGCGCGCGCGCGCGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCG 72
60  roProProLeuProProLeuProProLeuProProLeuTylValArgGlyAsn 76
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71  CGCGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCGCGCAAGCC 22
77  HisserThrGly 80
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21  CTGCGCACGGGC 10
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Db 1 MΩPFPYPOIT

QY 61 PPLPPLPPLPKRGHNSGTCLLVFEMVVALVGLGGMFOLFHLOKE----- 110  
DB 61 PPLPPLPPLPKRGHNSGTCLLVFEMVVALVGLGGMFOLFHLOKEELARESTSQ 120  
QY 111 PPLPPLPPLPKRGHNSGTCLLVFEMVVALVGLGGMFOLFHLOKEELARESTSQ 120  
DB 121 MHTASSLEKQIGHSPPEPEKELRKVAHLTGKSNSSMPLEWEDTYGIYLLSGVKKKGG 157  
QY 158 LVINETGLYFVYSKYVFRGSCNNLPLSHKVVYRNRSKYPDDLVMMEGKMMSYCTTGOMNA 217  
DB 181 LVINETGLYFVYSKYVFRGSCNNLPLSHKVVYRNRSKYPDDLVMMEGKMMSYCTTGOMNA 240  
QY 218 RSSYLGAVERNLTSAADHLVYVNSLSLVNFEESOTFFGLYKL 258  
DB 241 RSSYLGAVERNLTSAADHLVYVNSLSLVNFEESOTFFGLYKL 281

## RESULT 2

US-08-815-190A-2  
Sequence 2, Application US/08815190A  
Patent No. 6046310  
GENERAL INFORMATION:  
APPLICANT: Queen, Cary L.  
APPLICANT: Schneider, William P.  
APPLICANT: Vasquez, Maximiliano  
TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/815,190A  
FILING DATE: 11-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/614,584  
FILING DATE: 13-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 011823-006710US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-815-190A-2

Query Match 98.5%; Score 1389.5; DB 3; Length 281;  
Best Local Similarity 91.8%; Pred. No. 2.8e-100;  
Matches 258; Conservative 0; Mismatches 0; Indels 23; Gaps 1;  
QY 1 MOQPFNYPIQIYVWDSASSPMAAPGTIVLPCTSVPRRGQRPPPPPPPLPPPPPP 60  
DB 1 MOQPFNYPIQIYVWDSASSPMAAPGTIVLPCTSVPRRGQRPPPPPPPPPLPPPPPP 60  
QY 61 PPLPPLPPLPKRGHNSGTCLLVFEMVVALVGLGGMFOLFHLOKE----- 110

DB 61 PPLPPLPPLPKRGHNSGTCLLVFEMVVALVGLGGMFOLFHLOKEELARESTSQ 120  
QY 111 PPLPPLPPLPKRGHNSGTCLLVFEMVVALVGLGGMFOLFHLOKEELARESTSQ 157  
DB 121 MHTASSLEKQIGHSPPEPEKELRKVAHLTGKSNSSMPLEWEDTYGIYLLSGVKKKGG 180  
QY 158 LVINETGLYFVYSKYVFRGSCNNLPLSHKVVYRNRSKYPDDLVMMEGKMMSYCTTGOMNA 217  
DB 181 LVINETGLYFVYSKYVFRGSCNNLPLSHKVVYRNRSKYPDDLVMMEGKMMSYCTTGOMNA 240  
QY 218 RSSYLGAVERNLTSAADHLVYVNSLSLVNFEESOTFFGLYKL 258  
DB 241 RSSYLGAVERNLTSAADHLVYVNSLSLVNFEESOTFFGLYKL 281

## RESULT 3

US-09-290-640-25  
Sequence 25, Application US/09290640  
Patent No. 6204055  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Marcussen, Eric G.  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPh-0351  
CURRENT APPLICATION NUMBER: US/09/290,640  
CURRENT FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 25  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-290-640-25

Query Match 98.5%; Score 1389.5; DB 4; Length 281;  
Best Local Similarity 91.8%; Pred. No. 2.8e-100;  
Matches 258; Conservative 0; Mismatches 0; Indels 23; Gaps 1;  
QY 1 MOQPFNYPIQIYVWDSASSPMAAPGTIVLPCTSVPRRGQRPPPPPPPLPPPPPP 60  
DB 1 MOQPFNYPIQIYVWDSASSPMAAPGTIVLPCTSVPRRGQRPPPPPPPPPLPPPPPP 60  
QY 61 PPLPPLPPLPKRGHNSGTCLLVFEMVVALVGLGGMFOLFHLOKE----- 110  
DB 61 PPLPPLPPLPKRGHNSGTCLLVFEMVVALVGLGGMFOLFHLOKEELARESTSQ 120  
QY 111 PPLPPLPPLPKRGHNSGTCLLVFEMVVALVGLGGMFOLFHLOKEELARESTSQ 157  
DB 121 MHTASSLEKQIGHSPPEPEKELRKVAHLTGKSNSSMPLEWEDTYGIYLLSGVKKKGG 180  
QY 158 LVINETGLYFVYSKYVFRGSCNNLPLSHKVVYRNRSKYPDDLVMMEGKMMSYCTTGOMNA 217  
DB 181 LVINETGLYFVYSKYVFRGSCNNLPLSHKVVYRNRSKYPDDLVMMEGKMMSYCTTGOMNA 240  
QY 218 RSSYLGAVERNLTSAADHLVYVNSLSLVNFEESOTFFGLYKL 258  
DB 241 RSSYLGAVERNLTSAADHLVYVNSLSLVNFEESOTFFGLYKL 281

## RESULT 4

PCT-US95-00362-2  
Sequence 2, Application PC/TUS9500362  
GENERAL INFORMATION:  
APPLICANT: IMMUNEX CORPORATION  
TITLE OF INVENTION: Ligand That Binds Fas Antigen  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: US



ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/00362  
FILING DATE: 06-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/179,138  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/190,559  
FILING DATE: 01-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2805-WO  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-00362-2

Query Match 98.5%; Score 1389.5; DB 5; Length 281;  
Best Local Similarity 91.8%; Pred. No. 2.8e-100;  
Matches 258; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

QY 1 MOQPNYIPQIYWDSASSFWAPPGTVLPCPTSVPRRPGRRPPPPPPPLPPPPP 60  
DB 1 MOQPNYIPQIYWDSASSFWAPPGTVLPCPTSVPRRPGRRPPPPPPPLPPPPP 60  
QY 61 PPLPLPLPLKRRGNHSTGCLLVAFVAVLGLGIGMQLHLOKE----- 110  
DB 61 PPLPLPLPLKRRGNHSTGCLLVAFVAVLGLGIGMQLHLOKE----- 110  
QY 111 -----PSPPEKKELRKVAHLTGKSNRSMPLMEDYTGIVLLSGVYKKKG 157  
DB 121 MHTASLEKQIGHPPPEKKELRKVAHLTGKSNRSMPLMEDYTGIVLLSGVYKKKG 180  
QY 158 LVINETGLFYYSKYFFRGQSCNNPLPSHKYMYRNSKTIPODLVMEGKMMSCTTGOMMA 217  
DB 181 LVINETGLFYYSKYFFRGQSCNNPLPSHKYMYRNSKTIPODLVMEGKMMSCTTGOMMA 240  
QY 218 RSSYGAVERNLTSAHLYVNVSELVNFEESSQTFEGLYKL 258  
DB 241 RSSYGAVERNLTSAHLYVNVSELVNFEESSQTFEGLYKL 281

RESULT 5  
PCT-US95-00362-5  
Sequence 5, Application PC/TUS9500362  
GENERAL INFORMATION:  
APPLICANT: IMMUNEX CORPORATION  
TITLE OF INVENTION: Ligand That Binds Fas Antigen  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/00362  
FILING DATE: 06-JAN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/179,138  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/190,559  
FILING DATE: 01-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2805-WO  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 279 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-00362-5

Query Match 74.7%; Score 1053.5; DB 5; Length 279;  
Best Local Similarity 71.2%; Pred. No. 2.3e-74;  
Matches 200; Conservative 23; Mismatches 33; Indels 25; Gaps 3;

QY 1 MOQPNYIPQIYWDSASSFWAPPGTVLPCPTSVPRRPGRRPPPPPPPLPPPPP 60  
DB 1 MOQPNYIPQIYWDSASSFWAPPGTVLPCPTSVPRRPGRRPPPPPPPLPPPPP 60  
QY 61 PPLPLPLPLKRRGNHSTGCLLVAFVAVLGLGIGMQLHLOKE----- 110  
DB 61 PPLPLPLPLKRRGNHSTGCLLVAFVAVLGLGIGMQLHLOKE----- 110  
QY 111 -----PSPPEKKELRKVAHLTGKSNRSMPLMEDYTGIVLLSGVYKKKG 157  
DB 119 SLKVSFEKQINPSPPEKKELRKVAHLTGKSNRSMPLMEDYTGIVLLSGVYKKKG 178  
QY 158 LVINETGLFYYSKYFFRGQSCNNPLPSHKYMYRNSKTIPODLVMEGKMMSCTTGOMMA 217  
DB 179 LVINETGLFYYSKYFFRGQSCNNPLPSHKYMYRNSKTIPODLVMEGKMMSCTTGOMMA 238  
QY 218 RSSYGAVERNLTSAHLYVNVSELVNFEESSQTFEGLYKL 258  
DB 239 RSSYGAVERNLTSAHLYVNVSELVNFEESSQTFEGLYKL 279

RESULT 6  
US-08-751-512-8  
Sequence 8, Application US/08751512  
Patent No. 6001962  
GENERAL INFORMATION:  
APPLICANT: Ramer, J. Kevin  
APPLICANT: Williams, Lewis T.  
TITLE OF INVENTION: Modified FAS Ligands  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,512  
FILING DATE: 15-NOV-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, Matthew B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 02307K-07100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-751-512-8

Query Match 58.8%; Score 829; DB 3; Length 376;  
Best Local Similarity 68.4%; Pred. No. 6.5e-57;  
Matches 173; Conservative 3; Mismatches 25; Indels 52; Gaps 5;

QY 48 PPPPPPLPPPPPPPLPPLPLPKKRGK-----HSTGL---CL-----LVMFP 88  
DB 134 RAKPTTPRPRPRPTAPRTISQPLSLRPRACRPAGAVHTRGIDFACLEHHNHEFEY 133  
QY 89 MVLVALVGLGLGMPOLFLOKE-----PSPPEKKELRVAAH 125  
DB 194 M-----PMEOLFHLQKELAELERESTQMHNTASLEKQIGHPSPPPEKKELRVAAH 243  
QY 126 LTGKSNRSMPLMEDYGLVLLSGVYKKGGLVYNETGLFYYSKYFPGQSCNNPLPS 185  
DB 244 LTRKSNRSMPLMEDYGLVLLSGVYKKGGLVYNETGLFYYSKYFPGQSCNNPLPS 303  
QY 186 HKYMRNSKYPODLVMEGKMSYCTTGQMMARSSYLGAVERNLSADHLVYVSELSVN 245  
DB 304 HKYMRNSKYPODLVMEGKMSYCTTGQMMARSSYLGAVERNLSADHLVYVSELSVN 363  
QY 246 FEESQTFEGLYKL 258  
DB 364 FEESQTFEGLYKL 376

RESULT 7  
US-08-649-100-9  
Sequence 9, Application US/08649100  
Patent No. 6114507  
GENERAL INFORMATION:  
APPLICANT: SHIRAKAWA, KAMON  
APPLICANT: MATSUE, TOMOKAZU  
APPLICANT: NAGATA, SHIGEKAZU  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/649,100  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1110-160  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 179 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-649-100-9

Query Match 56.9%; Score 802.5; DB 4; Length 179;  
Best Local Similarity 87.2%; Pred. No. 3.3e-55;  
Matches 156; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

QY 103 QLFLOKE-----PSPPEKKELRVAAHLTGKSNRSMPLFW 139  
DB 1 QLFLOKELAELERESTQMHNTASLEKQIGHPSPPPEKKELRVAAHLTGKSNRSMPLFW 60  
QY 140 EDYTGIVLLSGVYKKGGLVYNETGLFYYSKYFPGQSCNNPLPSHKYMRNSKYPODL 199  
DB 61 EDYTGIVLLSGVYKKGGLVYNETGLFYYSKYFPGQSCNNPLPSHKYMRNSKYPODL 120  
QY 200 VMEGKMSYCTTGQMMARSSYLGAVERNLSADHLVYVSELSVNEESQTFEGLYKL 258  
DB 121 VMEGKMSYCTTGQMMARSSYLGAVERNLSADHLVYVSELSVNEESQTFEGLYKL 179

RESULT 8  
US-08-815-190A-16  
Sequence 16, Application US/08815190A  
Patent No. 6046310  
GENERAL INFORMATION:  
APPLICANT: Queen, Cary L.  
APPLICANT: Schneider, William P.  
APPLICANT: Vasquez, Maximiliano  
TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/815,190A  
FILING DATE: 11-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/614,584  
FILING DATE: 13-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 011823-0067100S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 287 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-815-190A-16

Query Match 56.9%; Score 802.5; DB 3; Length 287;  
Best Local Similarity 87.2%; Pred. No. 5.4e-55;  
Matches 156; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

103 QLFHOKK-----PSPPEKELKRVHLLTGKSNRSMPLM 139  
109 QLFHOKKLAELRESTSQMHTASSLEKIGSPSPPEKELKRVHLLTGKSNRSMPLM 168  
140 EDTYGVLLSGVKKYKKGGLVINEGLVYVSKYVFGOSCNPLPSHKYVMNSKYPODL 199  
169 EDTYGVLLSGVKKYKKGGLVINEGLVYVSKYVFGOSCNPLPSHKYVMNSKYPODL 228  
200 VMESGKMSYCTTGOMARRSYLGAVFNLTSADHLYVNVSELVNFESQTFEGLYKL 258  
229 VMESGKMSYCTTGOMARRSYLGAVFNLTSADHLYVNVSELVNFESQTFEGLYKL 287

## RESULT 9

US-08-584-031-17  
Sequence 17, Application US/08584031A

Patent No. 6030945  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
TITLE OF INVENTION: APO-2 LIGAND  
FILE REFERENCE: 11669.220503  
CURRENT APPLICATION NUMBER: US/08/584.031A  
CURRENT FILING DATE: 1996-01-09  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-584-031-17

Query Match 54.7%; Score 771.5; DB 3; Length 149;  
Best Local Similarity 99.3%; Pred. No. 6.6e-53;  
Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

111 PSPPEKELKRVHLLTGKSNRSMPLMEDIYGI-VLLSGYKRYKKGGLVINEGLYFY 169  
1 PSPPEKELKRVHLLTGKSNRSMPLMEDIYGI-VLLSGYKRYKKGGLVINEGLYFY 60  
170 SKYVFGOSCNPLPSHKYVMNSKYPODLVMEGKMSYCTTGOMARRSYLGAVFNL 229  
61 SKYVFGOSCNPLPSHKYVMNSKYPODLVMEGKMSYCTTGOMARRSYLGAVFNL 120  
230 SADHLYVNVSELVNFESQTFEGLYKL 258  
121 SADHLYVNVSELVNFESQTFEGLYKL 149

## RESULT 10

US-08-630-172-5  
Sequence 5, Application US/08630172

Patent No. 6060054  
GENERAL INFORMATION:  
APPLICANT: Staerz, Uwe  
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630.172  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-172-5

Query Match 53.7%; Score 758; DB 3; Length 145;  
Best Local Similarity 99.3%; Pred. No. 7e-52;  
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

114 PEKKEKELKRVHLLTGKSNRSMPLMEDIYGI-VLLSGYKRYKKGGLVINEGLYFY 173  
1 PEKKEKELKRVHLLTGKSNRSMPLMEDIYGI-VLLSGYKRYKKGGLVINEGLYFY 60  
174 FFGOSCNPLPSHKYVMNSKYPODLVMEGKMSYCTTGOMARRSYLGAVFNLTSADH 233  
61 FFGOSCNPLPSHKYVMNSKYPODLVMEGKMSYCTTGOMARRSYLGAVFNLTSADH 120  
234 LYVNVSELVNFESQTFEGLYKL 258  
121 LYVNVSELVNFESQTFEGLYKL 145

## RESULT 11

US-08-630-172-21  
Sequence 21, Application US/08630172

Patent No. 6060054  
GENERAL INFORMATION:  
APPLICANT: Staerz, Uwe  
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, 35th Floor  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630.172  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2879-36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 378 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-172-21

Query Match 53.7%; Score 758; DB 3; Length 378;  
Best Local Similarity 99.3%; Pred. No. 2e-51;  
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 114 PEKKELRKVAHLTGKSNRSMPLMEDTYGIVLLSGVKYKKGGLYINETGLGVYSKY 173  
DB 1 PEKKELRKVAHLTGKSNRSMPLMEDTYGIVLLSGVKYKKGGLYINETGLGVYSKY 60  
QY 174 FRGQSCNNLPLSHKRYMRNSKYPODLVMEGKMMSYCTTGOMARRSYLGAVENLTSADH 233  
DB 61 FRGQSCNNLPLSHKRYMRNSKYPODLVMEGKMMSYCTTGOMARRSYLGAVENLTSADH 120  
QY 234 LYVNSELSLVNEESQTFEGLYKL 258  
DB 121 LYVNSELSLVNEESQTFEGLYKL 145

## RESULT 12

PCT-US93-02475-13

Sequence 13, Application PC/TUS9302475  
GENERAL INFORMATION:

APPLICANT: Waisleski, Bernadine J.  
TITLE OF INVENTION: Tumor Necrosis Factor with Modified  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Donald G. Lewis  
STREET: 8328 Regents Road #1E  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage

COMPUTER: VE System 386  
OPERATING SYSTEM: MS-DOS 5  
SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/02475  
FILING DATE: 19930412

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/852,625

FILING DATE: 12 March 1992  
ATTORNEY/AGENT INFORMATION:

NAME: Donald G. Lewis  
REGISTRATION NUMBER: 28636  
REFERENCE/DOCKET NUMBER: BJW-2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2421

TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:  
LENGTH: 171 amino acids  
TYPE: AMINO ACIDS  
TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Lymphotoxin (murine)

OTHER INFORMATION: Two blank residues designated by

OTHER INFORMATION: "xaa" are inserted after residue No. 4 of murine

OTHER INFORMATION: Lymphotoxin and the sequence numbering is augmented

OTHER INFORMATION: by 2 starting with residue No. 5 in order to

OTHER INFORMATION: maximize the sequence homology with human  
OTHER INFORMATION: lymphotoxin.  
PUBLICATION INFORMATION:

AUTHORS: Li, C-B., Gray, R.W., Lin, P-F., McGrath,  
TITLE: Cloning and Expression of Murine  
JOURNAL: J. Immunology  
VOLUME: 138  
PAGES: 4496-4501

DATE: 1987  
RELEVANT RESIDUES IN SEQ ID NO: 13: 1-171 (includes  
RELEVANT RESIDUES IN SEQ ID NO: two blanks)  
PCT-US93-02475-13

Query Match 14.7%; Score 207; DB 5; Length 171;  
Best Local Similarity 31.4%; Pred. No. 2.7e-09;  
Matches 53; Conservative 28; Mismatches 78; Indels 10; Gaps 2;

QY 100 GMFQLEHLOKPEPPPEPK-----ELRKVAHLTGKSNRSMPLMEDTYGIVLLSGVKK 155  
DB 3 GVAXRFSAAHTAPLPOKHLTHGLKRAHLVGPQKNSLIRASTDRFLRHGSLSN 62  
QY 156 GGLVNETGLYEVYSKYVFGQSCN-----NPLSHKRYMRNSKYPODLVMEGKMMSY 209  
DB 63 NSLIPTSGLYFYVSQVFGSGESCPRAIPPTIYLAHEVOLFFSSQYFVHPLLSACKSVY 122  
QY 210 CTGOMARRSYLGAVENLTSADHLYVNSELSLVNEESQTFEGLYKL 258  
DB 123 PGIQFWVRSMYQGAVALSKGDLSTHTDGIHLHSPSVFGAFAL 171

## RESULT 13

US-08-855-825-14

Sequence 14, Application US/08855825  
Patent No. 6183951  
GENERAL INFORMATION:

APPLICANT: Plevy, Scott E.  
Targan, Stephen R.  
Taylor, Kent  
Barry, Mary J.

TITLE OF INVENTION: Methods of Diagnosing Clinical Subtypes  
of Crohn's Disease with Characteristic Responsiveness to  
Anti-Tnf Cytokine Therapy

NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego

STATE: California  
COUNTRY: United States  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/855,825  
FILING DATE: 12-May-1997  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-PM 2591

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 203 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

NAME/KEY: Lymphotoxin (murine)

OTHER INFORMATION: Two blank residues designated by

OTHER INFORMATION: "xaa" are inserted after residue No. 4 of murine

OTHER INFORMATION: Lymphotoxin and the sequence numbering is augmented

OTHER INFORMATION: by 2 starting with residue No. 5 in order to



Qy 122 KVAHLTGKSNRSRSMPLWEDTYGIVLLSGVKKYKGGVJINETGLYFVYSKYVFRGQ---- 177  
 Db 63 PAHLIGDPSKQKSLMRANTDRAFLQDGFSLNSLSLVPTSGIFYVSQVPSGKAYSP 122  
 Qy 178 --SCNNLPLSHKYVMRNSKYPQDDVMMEGKMSYCTTGOMMARRSYLGAVFNLTADHLY 235  
 Db 123 KATSSPLYLAHEVOLEFSQYPEHVPLLSQKMYVPGLOEPWLHSMYHGAFFOLTQGDOLS 182  
 Qy 236 VNVSELSLVNFEESQTFEGLYKL 258  
 Db 183 THTDGIPLHVLSPSTVFFGAFAL 205

Search completed: April 24, 2001, 15:31:52  
 Job time: 28 sec